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OM protein - protein search, using sw model

Run on: July 27, 2005, 03:27:05 ; Search time 43 Seconds

(without alignments)  
451.366 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECTGNGKNGYGTMSK.....TNSQVMEYCKIPSCDSRPV 260

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/1aa/6C\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/1aa/6D\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	100.0	260	4	US-09-982-516-1
2	1535	99.7	339	1	US-08-248-629A-3
3	1535	99.7	339	1	US-08-451-932-3
4	1535	99.7	339	1	US-08-452-260-3
5	1535	99.7	339	1	US-08-326-785-3
6	1535	99.7	339	2	US-08-612-788-3
7	1535	99.7	339	2	US-08-605-598B-3
8	1535	99.7	339	2	US-08-429-743-3
9	1535	99.7	339	2	US-08-866-735-3
10	1535	99.7	339	3	US-09-066-028-3
11	1535	99.7	339	4	US-09-335-325-3
12	1535	99.7	339	5	PCT-US95-05107-3
13	1535	99.7	374	3	US-09-377-250-2
14	1535	99.7	375	3	US-09-377-250-2
15	1535	99.7	378	2	US-08-612-788-42
16	1535	99.7	378	3	US-09-066-028-42
17	1535	99.7	378	4	US-09-335-325-42
18	1535	99.7	378	4	US-09-335-325-42
19	1535	99.7	451	3	US-09-377-250-1
20	1535	99.7	452	3	US-09-377-250-4
21	1535	99.7	790	1	US-08-469-486-54
22	1535	99.7	790	2	US-08-469-658-54
23	1535	99.7	791	1	US-08-643-219-1
24	1535	99.7	791	2	US-09-131-995-1
25	1535	99.7	791	2	US-08-832-087B-1
26	1535	99.7	791	3	US-08-851-350-1
27	1535	99.7	791	3	US-09-132-154-1

28	1535	99.7	791	4	US-08-991-761A-6	Sequence 6, Appli
29	1535	99.7	791	4	US-08-924-287A-1	Sequence 1, Appli
30	1535	99.7	810	1	US-07-854-603-2	Sequence 2, Appli
31	1535	99.7	810	1	US-08-147-000B-29	Sequence 29, Appli
32	1535	99.7	810	3	US-09-086-514-1	Sequence 1, Appli
33	1535	99.7	810	4	US-09-192-012-5	Sequence 5, Appli
34	1535	99.7	810	4	US-09-403-736-1	Sequence 1, Appli
35	1535	99.7	810	4	US-09-701-265-1	Sequence 1, Appli
36	1535	99.7	814	4	US-08-750-711-1	Sequence 1, Appli
37	1532	99.5	713	4	US-09-949-016-9983	Sequence 9983, Ap
38	1531	99.4	369	4	US-09-701-265-2	Sequence 2, Appli
39	1531	99.4	810	6	5200340-8	Patent No. 5200340
40	1531	99.4	810	6	5200340-8	Patent No. 5200340
41	1511	98.1	352	2	US-08-612-788-40	Sequence 40, Appli
42	1511	98.1	352	3	US-09-066-028-40	Sequence 40, Appli
43	1511	98.1	352	4	US-09-335-325-40	Sequence 40, Appli
44	1505	97.7	254	4	US-09-701-265-3	Sequence 3, Appli
45	1486	96.5	250	2	US-08-612-788-30	Sequence 30, Appli

## ALIGNMENTS

```
RESULT 1
US-09-982-516-1
Sequence 1, Application US/09982516
Patent No. 6723536
GENERAL INFORMATION:
APPLICANT: Madsen, John
APPLICANT: Liang, Hong
APPLICANT: Sim, Kim Lee
APPLICANT: Zhou, Xinhua
APPLICANT: Chang-Muxrad, Amy
APPLICANT: Boerner, Renee J.
APPLICANT: Boerner, Renee J.
APPLICANT: Mistry, Piroz R.
APPLICANT: Schrimsher, Jeffrey L.
APPLICANT: Shepard, Scott R.
TITLE OF INVENTION: Method of Producing and Purifying Angiostatin Protein
FILE REFERENCE: 05213-0562 43170-264313
CURRENT FILING DATE: 2002-09-10
CURRENT APPLICATION NUMBER: US/09/982,516
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PCT/US00/32843
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent version 3.1
SEQ ID NO 1
LENGTH: 260
TYPE: PRT
ORGANISM: Homo sapiens
US-09-982-516-1

Query Match 100.0%; Score 1540; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 3.3e-139;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECTGNGKNGYGTMSKSTGKNGITQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECTGNGKNGYGTMSKSTGKNGITQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
QY 61 DPGSPWCTTDPPEKRYDYCDILCEBECMHSGSENVGDKTSKMSGUECAWDSQSHAH 120
DB 61 DPGSPWCTTDPPEKRYDYCDILCEBECMHSGSENVGDKTSKMSGUECAWDSQSHAH 120
QY 121 GYIPSKFPNKLKKYCRNPDRELHPWCFTTDDNKWELCDIPRCTTTPPSGPTVQCLK 180
DB 121 GYIPSKFPNKLKKYCRNPDRELHPWCFTTDDNKWELCDIPRCTTTPPSGPTVQCLK 180
QY 181 GTGENTRGNAVTVSGTCHQMSAQTPHTHERTPENPCNLDENYCRNDGRRAPWCHT 240
DB 181 GTGENTRGNAVTVSGTCHQMSAQTPHTHERTPENPCNLDENYCRNDGRRAPWCHT 240
QY 240 GTGENTRGNAVTVSGTCHQMSAQTPHTHERTPENPCNLDENYCRNDGRRAPWCHT 240
DB 240 GTGENTRGNAVTVSGTCHQMSAQTPHTHERTPENPCNLDENYCRNDGRRAPWCHT 240
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Qy 241 TNSQVMEYCKIPSCDSSPV 260  
Db 241 TNSQVMEYCKIPSCDSSPV 260

## RESULT 2

US-08-248-629A-3  
Sequence 3, Application US/08248629A  
Patent No. 5639725

## GENERAL INFORMATION:

APPLICANT: Folkman, Judah  
APPLICANT: O'Reilly, Michael  
TITLE OF INVENTION: Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/248,629A  
FILING DATE: 04/26/94  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Larry W. Stults, Ph.D.  
REGISTRATION NUMBER: 34,025  
REFERENCE/DOCKET NUMBER: 05213-0120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-248-629A-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNGYGTMSKTNGITCKWSSSTSPHRRPSPATHPSBGLBENYCRNPND 60  
Db 1 VYLSECKTGNGKNGYGTMSKTNGITCKWSSSTSPHRRPSPATHPSBGLBENYCRNPND 60  
Qy 61 DPGSPWCYTTDPEKRYDYCDILIECEBCHGSGENYDGKISTMSGLBQAWDSOPHAH 120  
Db 61 DPGSPWCYTTDPEKRYDYCDILIECEBCHGSGENYDGKISTMSGLBQAWDSOPHAH 120  
Qy 121 GTIPSKFPKXNLKKNYCRNPDELPMWCTTDPNKRWELCDIPRCTTTPSSSGPTTYOCLK 180  
Db 121 GTIPSKFPKXNLKKNYCRNPDELPMWCTTDPNKRWELCDIPRCTTTPSSSGPTTYOCLK 180  
Qy 181 GTGENYRGNVAVTVSQHTQHSQAOTPHHTERTENPCNLDENYCRNPDGRAPWCHT 240  
Db 181 GTGENYRGNVAVTVSQHTQHSQAOTPHHTERTENPCNLDENYCRNPDGRAPWCHT 240  
Qy 241 TNSQVMEYCKIPSCDSSPV 260  
Db 241 TNSQVMEYCKIPSCDSSPV 260

## RESULT 3

US-08-451-932-3  
Sequence 3, Application US/08451932  
Patent No. 5733876

## GENERAL INFORMATION:

APPLICANT: Folkman, Judah  
APPLICANT: O'Reilly, Michael  
TITLE OF INVENTION: Method of Treating an Angiogenic  
Disease  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,932  
FILING DATE: 05/26/95  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/248,629  
FILING DATE: 04/26/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Larry W. Stults, Ph.D.  
REGISTRATION NUMBER: 34,025  
REFERENCE/DOCKET NUMBER: 05213-0123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-451-932-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNGYGTMSKTNGITCKWSSSTSPHRRPSPATHPSBGLBENYCRNPND 60  
Db 1 VYLSECKTGNGKNGYGTMSKTNGITCKWSSSTSPHRRPSPATHPSBGLBENYCRNPND 60  
Qy 61 DPGSPWCYTTDPEKRYDYCDILIECEBCHGSGENYDGKISTMSGLBQAWDSOPHAH 120  
Db 61 DPGSPWCYTTDPEKRYDYCDILIECEBCHGSGENYDGKISTMSGLBQAWDSOPHAH 120  
Qy 121 GTIPSKFPKXNLKKNYCRNPDELPMWCTTDPNKRWELCDIPRCTTTPSSSGPTTYOCLK 180  
Db 121 GTIPSKFPKXNLKKNYCRNPDELPMWCTTDPNKRWELCDIPRCTTTPSSSGPTTYOCLK 180  
Qy 181 GTGENYRGNVAVTVSQHTQHSQAOTPHHTERTENPCNLDENYCRNPDGRAPWCHT 240  
Db 181 GTGENYRGNVAVTVSQHTQHSQAOTPHHTERTENPCNLDENYCRNPDGRAPWCHT 240  
Qy 241 TNSQVMEYCKIPSCDSSPV 260  
Db 241 TNSQVMEYCKIPSCDSSPV 260

## RESULT 4

US-08-452-260-3  
Sequence 3, Application US/08452260  
Patent No. 5776704  
GENERAL INFORMATION:

APPLICANT: Folkman, Judah  
TITLE OF INVENTION: Method of Diagnosing an Angiogenic  
TITLE OF INVENTION: Disease  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,260  
FILING DATE: 05/26/95  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/248,629  
FILING DATE: 04/26/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Larry W. Scults, Ph.D.  
REGISTRATION NUMBER: 34,025  
REFERENCE/DOCKET NUMBER: 05213-0124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-452-260-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTNGKNRYGTMTKTKNGITCOKWSSTSPRRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTNGKNRYGTMTKTKNGITCOKWSSTSPRRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPOGWCCTTDPBKRYDYCDILECEBECMHGSGENYDGKISKTMSGLECOAWDSOPH 120  
DB 61 DPOGWCCTTDPBKRYDYCDILECEBECMHGSGENYDGKISKTMSGLECOAWDSOPH 120  
QY 121 GYIPSKFPKNLKKNYCRNPDRRLPWCFTTDPNKMELCDIPRCTPPSSGPTYOCLK 180  
DB 121 GYIPSKFPKNLKKNYCRNPDRRLPWCFTTDPNKMELCDIPRCTPPSSGPTYOCLK 180  
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 5  
US-08-326-785-3  
Sequence 3, Application US/08326785  
Patent No. 5792845  
GENERAL INFORMATION:  
APPLICANT: Folkman, Judah  
APPLICANT: O'Reilly, Michael  
TITLE OF INVENTION: Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/326,785  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/248,629  
FILING DATE: 04/26/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Larry W. Scults, Ph.D.  
REGISTRATION NUMBER: 34,025  
REFERENCE/DOCKET NUMBER: 05213-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-326-785-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTNGKNRYGTMTKTKNGITCOKWSSTSPRRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTNGKNRYGTMTKTKNGITCOKWSSTSPRRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPOGWCCTTDPBKRYDYCDILECEBECMHGSGENYDGKISKTMSGLECOAWDSOPH 120  
DB 61 DPOGWCCTTDPBKRYDYCDILECEBECMHGSGENYDGKISKTMSGLECOAWDSOPH 120  
QY 121 GYIPSKFPKNLKKNYCRNPDRRLPWCFTTDPNKMELCDIPRCTPPSSGPTYOCLK 180  
DB 121 GYIPSKFPKNLKKNYCRNPDRRLPWCFTTDPNKMELCDIPRCTPPSSGPTYOCLK 180  
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6  
US-08-612-788-3  
Sequence 3, Application US/08612788  
Patent No. 5837682  
GENERAL INFORMATION:  
APPLICANT: Folkman, W. Judah  
APPLICANT: O'Reilly, Michael  
APPLICANT: Cao, Yihai  
APPLICANT: Sim, B. Kim Lee  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia

COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
US-08-612-788-3

Query Match 99.7%; Score 1535; DB 2; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1,4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPRRPRSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPRRPRSPATHPSEGLEENYCRNPDN 60  
QY 61 DPGQWCYTTDPBKRKYDYCDILCEBECMHCSENYDGKISKTMGSLCQAMDSQSPHAA 120  
DB 61 DPGQWCYTTDPBKRKYDYCDILCEBECMHCSENYDGKISKTMGSLCQAMDSQSPHAA 120  
QY 121 GYIPSKFPNKLKKNYCRNPDELAPMCFTTDPNKRMLCDIPRCTTPPSSGPTTQCLK 180  
DB 121 GYIPSKFPNKLKKNYCRNPDELAPMCFTTDPNKRMLCDIPRCTTPPSSGPTTQCLK 180  
QY 181 GTGENYRGNAVAVTVSQHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPMCHT 240  
DB 181 GTGENYRGNAVAVTVSQHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPMCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 7  
US-08-605-598B-3  
Sequence 3, Application US/08605598B  
Patent No. 5861372  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
APPLICANT: Lin, Jie  
APPLICANT: O'Reilly, Michael S.  
TITLE OF INVENTION: Aggregating Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta

STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,598B  
FILING DATE: 22-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Human Angiostatin  
US-08-605-598B-3

Query Match 99.7%; Score 1535; DB 2; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1,4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPRRPRSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPRRPRSPATHPSEGLEENYCRNPDN 60  
QY 61 DPGQWCYTTDPBKRKYDYCDILCEBECMHCSENYDGKISKTMGSLCQAMDSQSPHAA 120  
DB 61 DPGQWCYTTDPBKRKYDYCDILCEBECMHCSENYDGKISKTMGSLCQAMDSQSPHAA 120  
QY 121 GYIPSKFPNKLKKNYCRNPDELAPMCFTTDPNKRMLCDIPRCTTPPSSGPTTQCLK 180  
DB 121 GYIPSKFPNKLKKNYCRNPDELAPMCFTTDPNKRMLCDIPRCTTPPSSGPTTQCLK 180  
QY 181 GTGENYRGNAVAVTVSQHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPMCHT 240  
DB 181 GTGENYRGNAVAVTVSQHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPMCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 8  
US-08-429-743-3  
Sequence 3, Application US/08429743  
Patent No. 5885795  
GENERAL INFORMATION:  
APPLICANT: O'Reilly, Michael  
APPLICANT: Folkman, M. Judah  
APPLICANT: Sim, Kim Lee  
APPLICANT: Cao, Yihai  
TITLE OF INVENTION: Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,743
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,629
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,785
FILING DATE: 20-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, James D.
REGISTRATION NUMBER: 31,771
REFERENCE/DOCKET NUMBER: 05213-0122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ORIGINAL SOURCE: NO
ORGANISM: Homo sapiens
US-08-429-743-3

Query Match          99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No.-1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTMSKTKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNGYGTMSKTKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPQPGWCYTTDPKRYDYCDILCEBECMHCSGSENYDGKISKTMGSLGECQAMDSQSPHAA 120
DB 61 DPQPGWCYTTDPKRYDYCDILCEBECMHCSGSENYDGKISKTMGSLGECQAMDSQSPHAA 120
QY 121 GYISKFPKPKLKKYCRNPDRRLRPMCFCTTDPKRWELCDIPRCTTPPSSSGPTYOCLK 180
DB 121 GYISKFPKPKLKKYCRNPDRRLRPMCFCTTDPKRWELCDIPRCTTPPSSSGPTYOCLK 180
QY 181 GTGSENYGNVAVTYSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGSENYGNVAVTYSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 9
US-08-866-735-3
Sequence 3, Application US/08866735
Patent No. 5945403
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
```

```
COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,735
FILING DATE: 30-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
US-08-866-735-3

Query Match          99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No.-1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTMSKTKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNGYGTMSKTKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPQPGWCYTTDPKRYDYCDILCEBECMHCSGSENYDGKISKTMGSLGECQAMDSQSPHAA 120
DB 61 DPQPGWCYTTDPKRYDYCDILCEBECMHCSGSENYDGKISKTMGSLGECQAMDSQSPHAA 120
QY 121 GYISKFPKPKLKKYCRNPDRRLRPMCFCTTDPKRWELCDIPRCTTPPSSSGPTYOCLK 180
DB 121 GYISKFPKPKLKKYCRNPDRRLRPMCFCTTDPKRWELCDIPRCTTPPSSSGPTYOCLK 180
QY 181 GTGSENYGNVAVTYSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGSENYGNVAVTYSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 10
US-09-066-028-3
Sequence 3, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
```

CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/066,028  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/612,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
US-09-066-028-3

Query Match 99.7%; Score 1535; DB 3; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1,4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKMSSTSPHRRFSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKMSSTSPHRRFSPATHPSEGLEENYCRNPDN 60  
QY 61 DPGPWCYTTDPDEKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAMDOSQSPHAA 120  
DB 61 DPGPWCYTTDPDEKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAMDOSQSPHAA 120  
QY 121 GYIPSKFPKKNLKKYCNRPDLRPMWCTTDPNKRWELCDIPRCTTTPPPSSGPTVQCLK 180  
DB 121 GYIPSKFPKKNLKKYCNRPDLRPMWCTTDPNKRWELCDIPRCTTTPPPSSGPTVQCLK 180  
QY 181 GTGENYRGNAVAVTVSGHTCQHMSAQTPTHRTPEHPCKNLDENYCRNPDGKRAFWCHT 240  
DB 181 GTGENYRGNAVAVTVSGHTCQHMSAQTPTHRTPEHPCKNLDENYCRNPDGKRAFWCHT 240  
QY 241 TNSQVWEYCKIIPSCDSSPV 260  
DB 241 TNSQVWEYCKIIPSCDSSPV 260

## RESULT 11

US-09-335-325-3  
Sequence 3, Application US/09335325  
Patent No. 6521439  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
O'Reilly, Michael  
Cao, Yihai  
Sim, B. Kim Lee

TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/335,325  
FILING DATE: 17-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-335-325-3

Query Match 99.7%; Score 1535; DB 4; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1,4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKMSSTSPHRRFSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKMSSTSPHRRFSPATHPSEGLEENYCRNPDN 60  
QY 61 DPGPWCYTTDPDEKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAMDOSQSPHAA 120  
DB 61 DPGPWCYTTDPDEKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAMDOSQSPHAA 120  
QY 121 GYIPSKFPKKNLKKYCNRPDLRPMWCTTDPNKRWELCDIPRCTTTPPPSSGPTVQCLK 180  
DB 121 GYIPSKFPKKNLKKYCNRPDLRPMWCTTDPNKRWELCDIPRCTTTPPPSSGPTVQCLK 180  
QY 181 GTGENYRGNAVAVTVSGHTCQHMSAQTPTHRTPEHPCKNLDENYCRNPDGKRAFWCHT 240  
DB 181 GTGENYRGNAVAVTVSGHTCQHMSAQTPTHRTPEHPCKNLDENYCRNPDGKRAFWCHT 240  
QY 241 TNSQVWEYCKIIPSCDSSPV 260  
DB 241 TNSQVWEYCKIIPSCDSSPV 260

## RESULT 12

PCT-US95-05107-3  
Sequence 3, Application PC/TUS9505107

GENERAL INFORMATION:  
APPLICANT: THE CHILDREN'S MEDICAL CENTER, CORPORATION  
TITLE OF INVENTION: Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Akeaw  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05107  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,629  
FILING DATE: 26-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/326,785  
FILING DATE: 20-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Johnson, James D.  
REGISTRATION NUMBER: 31,771  
REFERENCE/DOCKET NUMBER: 05213-0122  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PCT-US95-05107-3

Query Match 99.7%; Score 1535; DB 5; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTMSKTNGITCOKWSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYGTMSKTNGITCOKWSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPOGWCYTTDPKRYDYCDILECEECHGSGENYDGKISKTMGLECOAMDQSPHAA 120  
DB 61 DPOGWCYTTDPKRYDYCDILECEECHGSGENYDGKISKTMGLECOAMDQSPHAA 120  
QY 121 GYIPSKFPKNNLKKYCNCRNDRRLRPMCTTDPNKKWELCDIPRCTTPPSSGPTYQCLK 180  
DB 121 GYIPSKFPKNNLKKYCNCRNDRRLRPMCTTDPNKKWELCDIPRCTTPPSSGPTYQCLK 180  
QY 181 GTGENTRGNAVAATVSGHTCOHWSAOTPHHTERTPENPCNDENYCNPDGKRAPWCHT 240  
DB 181 GTGENTRGNAVAATVSGHTCOHWSAOTPHHTERTPENPCNDENYCNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 13  
US-09-377-250-3  
; Sequence 3, Application us/09377250

Patent No. 6365364  
GENERAL INFORMATION:  
APPLICANT: MANN, KENNETH G.  
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF  
FILE REFERENCE: 48409/360  
CURRENT APPLICATION NUMBER: US/09/377,250  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 3  
LENGTH: 374  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: angiogenesis inhibitor  
NAME/KEY: MOD.RES  
LOCATION: (264)  
OTHER INFORMATION: Xaa = Gln or Glu  
US-09-377-250-3

Query Match 99.7%; Score 1535; DB 3; Length 374;  
Best Local Similarity 99.6%; Pred. No. 1.6e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTMSKTNGITCOKWSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYGTMSKTNGITCOKWSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPOGWCYTTDPKRYDYCDILECEECHGSGENYDGKISKTMGLECOAMDQSPHAA 120  
DB 61 DPOGWCYTTDPKRYDYCDILECEECHGSGENYDGKISKTMGLECOAMDQSPHAA 120  
QY 121 GYIPSKFPKNNLKKYCNCRNDRRLRPMCTTDPNKKWELCDIPRCTTPPSSGPTYQCLK 180  
DB 121 GYIPSKFPKNNLKKYCNCRNDRRLRPMCTTDPNKKWELCDIPRCTTPPSSGPTYQCLK 180  
QY 181 GTGENTRGNAVAATVSGHTCOHWSAOTPHHTERTPENPCNDENYCNPDGKRAPWCHT 240  
DB 181 GTGENTRGNAVAATVSGHTCOHWSAOTPHHTERTPENPCNDENYCNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 14  
US-09-377-250-2  
; Sequence 2, Application us/09377250  
Patent No. 6365364  
GENERAL INFORMATION:  
APPLICANT: MANN, KENNETH G.  
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF  
FILE REFERENCE: 48409/360  
CURRENT APPLICATION NUMBER: US/09/377,250  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 375  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: angiogenesis inhibitor  
NAME/KEY: MOD.RES  
LOCATION: (265)  
OTHER INFORMATION: Xaa = Gln or Glu  
US-09-377-250-2

Query Match 99.7%; Score 1535; DB 3; Length 375;

Best Local Similarity 99.6%; Pred. No. 1.6e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 VILSECKTGNGKXRYGTMSKTXNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
Db 2 VILSECKTGNGKXRYGTMSKTXNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 61  
Qy 61 DPGPWCYTTDPKRYDYCDILECEBECNHCSENYDGIKSTMSGLECQAMDSQSPH 120  
Db 62 DPGPWCYTTDPKRYDYCDILECEBECNHCSENYDGIKSTMSGLECQAMDSQSPH 121  
Qy 121 GYIPSKFPNKNLKNYCRNPDRELPRWCFTTDPNKRWEICDI PRCTTTPSSGPTYQCLK 180  
Db 122 GYIPSKFPNKNLKNYCRNPDRELPRWCFTTDPNKRWEICDI PRCTTTPSSGPTYQCLK 181  
Qy 181 GTGENTRGNAVAVTSGHTCQHSAGTPTHTERTPENPCNIDENYCRNPDGRAPWCHT 240  
Db 182 GTGENTRGNAVAVTSGHTCQHSAGTPTHTERTPENPCNIDENYCRNPDGRAPWCHT 241  
Qy 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 242 TNSQVRWEYCKIPSCDSSPV 261

RESULT 15  
US-08-612-788-42  
Sequence 42, Application US/08612788  
Patent No. 5637682  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
APPLICANT: O'Reilly, Micheal  
APPLICANT: Cao, Yihai  
APPLICANT: Sim, B. Kim Lee  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 378 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEetical: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: K1-4BRLS  
US-08-612-788-42

Query Match 99.7%; Score 1535; DB 2; Length 378;  
Best Local Similarity 99.6%; Pred. No. 1.6e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 VILSECKTGNGKXRYGTMSKTXNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
Db 6 VILSECKTGNGKXRYGTMSKTXNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 65  
Qy 61 DPGPWCYTTDPKRYDYCDILECEBECNHCSENYDGIKSTMSGLECQAMDSQSPH 120  
Db 66 DPGPWCYTTDPKRYDYCDILECEBECNHCSENYDGIKSTMSGLECQAMDSQSPH 125  
Qy 121 GYIPSKFPNKNLKNYCRNPDRELPRWCFTTDPNKRWEICDI PRCTTTPSSGPTYQCLK 180  
Db 126 GYIPSKFPNKNLKNYCRNPDRELPRWCFTTDPNKRWEICDI PRCTTTPSSGPTYQCLK 185  
Qy 181 GTGENTRGNAVAVTSGHTCQHSAGTPTHTERTPENPCNIDENYCRNPDGRAPWCHT 240  
Db 186 GTGENTRGNAVAVTSGHTCQHSAGTPTHTERTPENPCNIDENYCRNPDGRAPWCHT 245  
Qy 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 246 TNSQVRWEYCKIPSCDSSPV 265

Search completed: July 27, 2005, 03:31:19  
Job time: 45 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 03:18:29 ; Search time 73 seconds  
(without alignments)  
1377.503 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540  
Sequence: 1 VYLSECKTNGKNYRGIMSK.....TNSQVWEXYCKIPSCDSPV 260

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: geneseqp1808:.\*  
2: geneseqp1908:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	100.0	260	3 AAB26486	AAB26486 Deglycosy
2	1540	100.0	260	4 AAU01209	AAU01209 Human Ang
3	1537	99.8	869	7 ADK40316	ADK40316 C-termina
4	1537	99.8	869	7 ADK40314	ADK40314 N-termina
5	1535	99.7	260	6 AAG79748	AAG79748 Human pla
6	1535	99.7	268	2 AAU02109	AAU02109 A multifu
7	1535	99.7	285	2 AAU02102	AAU02102 A multifu
8	1535	99.7	339	2 AAR83961	AAR83961 Human pla
9	1535	99.7	339	2 AAU07581	AAU07581 N-Termina
10	1535	99.7	339	2 AAU94038	AAU94038 Human ang
11	1535	99.7	339	4 AAU50518	AAU50518 Human ang
12	1535	99.7	339	7 ADG47024	ADG47024 Human ang
13	1535	99.7	339	8 ADM11543	ADM11543 Human pla
14	1535	99.7	363	3 AAU70255	AAU70255 Human ang
15	1535	99.7	364	2 AAU02106	AAU02106 A multifu
16	1535	99.7	374	3 AAU79226	AAU79226 Angiogene
17	1535	99.7	375	3 AAU79225	AAU79225 Angiogene
18	1535	99.7	378	2 AAU75729	AAU75729 Human kri
19	1535	99.7	378	3 AAB16450	AAB16450 Human ang
20	1535	99.7	378	5 AAU48894	AAU48894 Human ang
21	1535	99.7	378	7 ADG47063	ADG47063 Human ang
22	1535	99.7	380	2 AAU02105	AAU02105 A multifu
23	1535	99.7	381	2 AAU02101	AAU02101 A multifu
24	1535	99.7	391	6 ADA08454	ADA08454 Mammalian
25	1535	99.7	391	8 ADP67426	ADP67426 A61 anti-

26	1535	99.7	394	6 ADA08455	ADA08455 Mammalian
27	1535	99.7	394	8 ADP67427	ADP67427 A61 anti-
28	1535	99.7	452	3 AAU79224	AAU79224 Angiogene
29	1535	99.7	453	3 AAU02093	AAU02093 A multifu
30	1535	99.7	453	2 AAU02099	AAU02099 A multifu
31	1535	99.7	453	2 AAU02095	AAU02095 A multifu
32	1535	99.7	453	2 AAU02096	AAU02096 A multifu
33	1535	99.7	453	2 AAU95051	AAU95051 Amino aci
34	1535	99.7	470	2 AAU02112	AAU02112 A multifu
35	1535	99.7	480	7 ABU64288	ABU64288 Human ang
36	1535	99.7	484	6 AAG79749	AAG79749 Human pla
37	1535	99.7	563	5 ABB75942	ABB75942 Endothe
38	1535	99.7	566	2 AAU02100	AAU02100 A multifu
39	1535	99.7	571	5 ABB75944	ABB75944 Angiotens
40	1535	99.7	576	5 ABB75943	ABB75943 Angiotens
41	1535	99.7	579	8 ADG82532	ADG82532 Pro lactin
42	1535	99.7	654	8 ABM83810	ABM83810 Human dia
43	1535	99.7	672	8 ABM83809	ABM83809 Human dia
44	1535	99.7	714	7 ABG75025	ABG75025 Lys-plasm
45	1535	99.7	790	2 AAR60519	AAR60519 Human 'G1

## ALIGNMENTS

RESULT 1	AAB26486	standard; protein; 260 AA.
ID	AAB26486	
XX	AAB26486	
AC	AAB26486	
XX	AAB26486	
DT	16-JAN-2001	(first entry)
XX		
DE	Deglycosylated kringle 1-5 region protein.	
XX		
KW	Deglycosylated; kringle; angiogenesis; human.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200047729-A1.	
XX		
PD	17-AUG-2000.	
XX		
PF	10-FEB-2000; 2000WO-US003482.	
XX		
PR	10-FEB-1999; 99US-0119562P.	
XX		
PR	07-APR-1999; 99US-0128062P.	
XX		
PA	(ENTR-) ENTREMED INC.	
XX	(CHIL-) CHILDRENS MEDICAL CENT.	
PI	Pitie-Shepherd S, Folkman MJ, Liang H, Macdonald NU, Sim KL;	
XX	WPI; 2000-579032/54.	
DR	N-PSDB; AAA94906.	
XX		
PT	Novel composition comprising deglycosylated fragments of kringle 1-5	
XX	regions of plasminogen linked to the glycosylated form, useful for	
PT	inhibiting angiogenesis.	
XX		
PS	Claim 7; Fig 1; 42PP; English.	
XX		
CC	The present sequence is deglycosylated kringle 1-5 region protein.	
XX	Deglycosylated kringle 1-5 region protein has increased antiangiogenic	
CC	activity as compared to glycosylated kringle 1-5 region protein. The	
XX	deglycosylated kringle 1-5 region protein was isolated from human	
CC	plasminogen by affinity chromatography	
XX		
SO	Sequence 260 AA;	
XX		
Query Match	100.0%;	Score 1540; DB 3; Length 260;
Best Local Similarity	100.0%;	Pred. No. 8.7e-91;
Matches 260; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;



XX Disclosure; Fig 8; 136bp; English.  
PS  
XX  
CC The invention relates to an albumin fusion protein comprising an  
CC angiogenesis inhibiting peptide and an albumin having an albumin  
CC activity, or their fragments or variants. The albumin fusion proteins,  
CC compositions, vaccines and methods are useful for treating angiogenesis-  
CC dependent tumor, e.g. cancer. This sequence represents an C-terminal  
CC albumin-angiotensin fusion protein.  
SQ  
SQ Sequence 869 AA;  
Query Match 99.8%; Score 1537; DB 7; Length 869;  
Best Local Similarity 99.6%; Pred. No. 4.2e-90;  
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNKNGRTGMSKTNGITCQKMSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
DB 610 VYLSECKTGNKNGRTGMSKTNGITCQKMSSTSPHPRPSPATHPSEGLEENYCRNPDN 669  
QY 61 DPGPWCYTTDPKRYDYCDILCEBECMHCSENYDGKISKTMSEGCQAMDSQSPH 120  
DB 670 DPGPWCYTTDPKRYDYCDILCEBECMHCSENYDGKISKTMSEGCQAMDSQSPH 729  
QY 121 GYISKEPNKYLKKNYCRNPDRELPRWCFTTDPNKMELCDIPRCTPPSSGPTYOCLK 180  
DB 730 GYISKEPNKYLKKNYCRNPDRELPRWCFTTDPNKMELCDIPRCTPPSSGPTYOCLK 789  
QY 181 GTGENYGNVAVTSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGRAPWCHT 240  
DB 790 GTGENYGNVAVTSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGRAPWCHT 849  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 850 TNSQVRWEYCKIPSCDSSPV 869  
RESULT 4  
ADK40314  
ID ADK40314 standard; protein; 869 AA.  
AC ADK40314;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE N-terminal angiotensin-albumin fusion protein.  
XX  
KW cytosolic; vaccine; albumin fusion protein;  
KW angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer;  
KW collagen.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO2003066085-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 07-FEB-2003; 2003WO-IB000433.  
XX  
PR 07-FEB-2002; 2002US-0355547P.  
XX  
PA (AVET) AVENTIS BEHRING GMBH.  
PA (DELZ) DELTA BIOTECHNOLOGY LTD.  
PI Mertine P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;  
XX WPI: 2003-731479/69.  
DR N-PSDB; ADK40313.  
XX  
PT New albumin fusion protein comprising an angiogenesis inhibiting peptide  
PT and an albumin having an albumin activity, or their fragments or  
PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.

XX Disclosure; Fig 6; 136bp; English.  
PS  
XX  
CC The invention relates to an albumin fusion protein comprising an  
CC angiogenesis inhibiting peptide and an albumin having an albumin  
CC activity, or their fragments or variants. The albumin fusion proteins,  
CC compositions, vaccines and methods are useful for treating angiogenesis-  
CC dependent tumor, e.g. cancer. This sequence represents an N-terminal  
CC angiotensin-albumin fusion protein.  
SQ  
SQ Sequence 869 AA;  
Query Match 99.8%; Score 1537; DB 7; Length 869;  
Best Local Similarity 99.6%; Pred. No. 4.2e-90;  
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNKNGRTGMSKTNGITCQKMSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
DB 25 VYLSECKTGNKNGRTGMSKTNGITCQKMSSTSPHPRPSPATHPSEGLEENYCRNPDN 84  
QY 61 DPGPWCYTTDPKRYDYCDILCEBECMHCSENYDGKISKTMSEGCQAMDSQSPH 120  
DB 85 DPGPWCYTTDPKRYDYCDILCEBECMHCSENYDGKISKTMSEGCQAMDSQSPH 144  
QY 121 GYISKEPNKYLKKNYCRNPDRELPRWCFTTDPNKMELCDIPRCTPPSSGPTYOCLK 180  
DB 145 GYISKEPNKYLKKNYCRNPDRELPRWCFTTDPNKMELCDIPRCTPPSSGPTYOCLK 204  
QY 181 GTGENYGNVAVTSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGRAPWCHT 240  
DB 205 GTGENYGNVAVTSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGRAPWCHT 264  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 265 TNSQVRWEYCKIPSCDSSPV 284  
RESULT 5  
AAG79748  
ID AAG79748 standard; protein; 260 AA.  
AC AAG79748;  
XX  
DT 18-MAR-2003 (first entry)  
XX  
DE Human plasminogen kringle domains 1-3, KL-3.  
XX  
KW Human; plasminogen; angiotensin; neovascularisation; kringle domain;  
KW cell proliferation; viral vector; replication-defective; cancer; tumour.  
XX  
OS Homo sapiens.  
OS  
PN WO200288173-A2.  
XX  
PD 07-NOV-2002.  
XX  
PF 29-APR-2002; 2002WO-US013461.  
XX  
PR 30-APR-2001; 2001US-0287673P.  
PR 05-APR-2002; 2002US-0370634P.  
XX  
PA (CELL-) CELL GENESYS INC.  
PI Chang B, Wu WW, MacArthur J, Patel S, Joos K, Mendez M;  
XX WPI: 2003-129131/12.  
DR N-PSDB; ABA00776.  
XX  
PT New recombinant viral vector expressing human angiotensin useful for  
PT inhibiting angiogenesis in a mammalian subject with cancer or tumor.  
PS Disclosure; Page 75-76; 83pp; English.



XX	02-NOV-1995.
XX	
XX	26-APR-1995; 95WO-US005107.
XX	
XX	26-APR-1994; 94US-00248629.
PR	20-OCT-1994; 94US-00326785.
XX	
PA	(CHIL-) CHILDRENS MEDICAL CENT.
XX	
PI	O'Reilly MS, Folkman MJ, Sim KL, Cao Y;
XX	
DR	WPI; 1995-382990/49.
PT	Endothelial inhibitor Angiostatin - useful to treat angiogenic mediated
XX	disease esp. angiogenesis and cancer.
XX	
PS	Claim 4; Page 81-82; 108pp; English.
XX	
CC	The sequence represents a plasminogen fragment which is compared with the
CC	corresponding plasminogen fragments of monkey (AAR83962), pig (AAR83963)
CC	and cattle (AAR83964) origin (in Fig.2), as well as the with the first
CC	339 amino acids of mouse angiostatin (AAR83960) (i.e. aa's 98-436 of the
CC	complete 812 aa plasminogen molecule AAR83959). Human angiostatin is a
CC	plasminogen fragment starting at aa 97 or 99 of the complete plasminogen
CC	molecule. Angiostatin is an endothelial inhibitor, which reversibly
CC	inhibits proliferation of endothelial cells and thereby inhibits
CC	angiogenesis. It is useful in the treatment of a human or animal with
CC	angiogenic mediated disease e.g. arthritis, macular degeneration,
CC	diabetic retinopathy or cancer. Cells comprising angiostatin-coding
CC	sequences are useful for gene therapy of primary tumours.

**SQ Sequence 339 AA;**

Query Match 99.7%; Score 1535; DB 2: Length 339.

Best Local Similarity 99.6%; Pred: No. 2.3e-90;  
Matches 259: Conservative 0: Mismatches 1: Indels 0: Gaps 0

1

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

1 123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100101102103104105106107108109110111112113114115116117118119120121122123124125126127128129130131132133134135136137138139140141142143144145146147148149150151152153154155156157158159160161162163164165166167168169170171172173174175176177178179180181182183184185186187188189190191192193194195196197198199200201202203204205206207208209210211212213214215216217218219220221222223224225226227228229230231232233234235236237238239240241242243244245246247248249250251252253254255256257258259260261262263264265266267268269270271272273274275276277278279280281282283284285286287288289290291292293294295296297298299300301302303304305306307308309310311312313314315316317318319320321322323324325326327328329330331332333334335336337338339340341342343344345346347348349350351352353354355356357358359360361362363364365366367368369370371372373374375376377378379380381382383384385386387388389390391392393394395396397398399400401402403404405406407408409410411412413414415416417418419420421422423424425426427428429430431432433434435436437438439440441442443444445446447448449450451452453454455456457458459460461462463464465466467468469470471472473474475476477478479480481482483484485486487488489490491492493494495496497498499500501502503504505506507508509510511512513514515516517518519520521522523524525526527528529530531532533534535536537538539540541542543544545546547548549550551552553554555556557558559560561562563564565566567568569570571572573574575576577578579580581582583584585586587588589590591592593594595596597598599600601602603604605606607608609610611612613614615616617618619620621622623624625626627628629630631632633634635636637638639640641642643644645646647648649650651652653654655656657658659660661662663664665666667668669670671672673674675676677678679680681682683684685686687688689690691692693694695696697698699700701702703704705706707708709710711712713714715716717718719720721722723724725726727728729730731732733734735736737738739740741742743744745746747748749750751752753754755756757758759760761762763764765766767768769770771772773774775776777778779780781782783784785786787788789790791792793794795796797798799800801802803804805806807808809810811812813814815816817818819820821822823824825826827828829830831832833834835836837838839840841842843844845846847848849850851852853854855856857858859860861862863864865866867868869870871872873874875876877878879880881882883884885886887888889890891892893894895896897898899900901902903904905906907908909910911912913914915916917918919920921922923924925926927928929930931932933934935936937938939940941942943944945946947948949950951952953954955956957958959960961962963964965966967968969970971972973974975976977978979980981982983984985986987988989990991992993994995996997998999100010011002100310041005100610071008100910101011101210131014101510161017101810191020102110221023102410251026102710281029103010311032103310341035103610371038103910401041104210431044104510461047104810491050105110521053105410551056105710581059106010611062106310641065106610671068106910701071107210731074107510761077107810791080108110821083108410851086108710881089109010911092109310941095109610971098109911001101110211031104110511061107110811091110111111121113111411151116111711181119112011211122112311241125112611271128112911301131113211331134113511361137113811391140114111421143114411451146114711481149115011511152115311541155115611571158115911601161116211631164116511661167116811691170117111721173117411751176117711781179118011811182118311841185118611871188118911901191119211931194119511961197119811991200120112021203120412051206120712081209121012111212121312141215121612171218121912201221122212231224122512261227122812291230123112321233123412351236123712381239124012411242124312441245124612471248124912501251125212531254125512561257125812591260126112621263126412651266126712681269127012711272127312741275127612771278127912801281128212831284128512861287128812891290129112921293129412951296129712981299130

61 DPQGPWCYTTDPEKRYDYCDILECEECECMHCSGENYDGIKSTMSGLECAWDSQSPHAI

61 DPQGPWCYTTDPDKRYDYCDILECEEECHSCGENYDGKISKTMGSGLECGAWDSQSPHAH 12

121 GYPSKFPNKLKKNYCRNPDRRLRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYOCJK 18

Db  
121 GYIPSEPNKYLKQNYCRNPDEI.BPWCETTPDNKRWEI.CDI.BRCTTPBPSSCPTVOCI.K.1.6

[illegible]

100

CONFIDENTIAL

411 INSQVNMELCNI FSLDSSPV 260

DB 241 TNSQVRMEYCKIPSCDSSPV 260

**53311**

AAW07581

XX ID AAWU/581 standard; protein; 339 AA.

AC AAW07581;  
XY

DT 24-JUN-1997 (first entry)

DE N-Terminal angiotstatin fragment.

**KW** angiotensin: n]asminogen: kring]: angiotensin: angiotensin: angiotensin:

macular degeneration; diabetic retinopathy.

OS Homo sapiens.

```

XX XX WO9635774-A2.
XX DE
XX XX 14-NOV-1996.
XX PD
XX XX 26-APR-1996; 96WO-US005856.
XX PF
XX XX 26-APR-1995; 95US-00429743.
XX PR 22-FEB-1996; 96US-00605598.
XX PR 08-MAR-1996; 96US-00612788.
XX XX
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Folkman MJ, O'Reilly MS, Cao Y, Sim KL, Lin J;
XX DR WPI; 1996-518662/51.
XX XX
XX PT Use of angiotastatin fragments or aggregates - for inhibiting endothelial
XX PT cell proliferation and treating angiogenesis-mediated diseases, e.g.
XX PT cancer, arthritis or diabetic retinopathy.
XX PS
XX PS Claim 59; Page 96-97; 203pp; English.
XX CC
XX CC The invention relates to new methods and compositions for inhibiting
XX CC endothelial cell proliferation, using as active component an angiotastatin
XX CC fragment, a combination of angiotastatin fragments, or aggregate
XX CC angiotastatin. The fragment is preferably derived from murine, human,
XX CC Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2,
XX CC kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle 1-4 or kringle
XX CC 1-4BKS protein. The aggregate angiotastatin has a Mol. Wt. of 45-65 kD and
XX CC is derived from a plasminogen fragment beginning at approximately amino
XX CC acid number 98 of murine, human, Rhesus, porcine or bovine plasminogen.
XX CC The active component can be used for treating angiogenesis-mediated
XX CC diseases such as cancer, arthritis, macular degeneration and diabetic
XX CC retinopathy. It can also be used to develop antibodies for use in
XX CC diagnosis, detection and therapy. The present sequence, which is the N-
XX CC terminal fragment of human angiotastatin, is a specific aggregate
XX CC angiotastatin which can be used in the invention
XX SQ
XX Sequence 339 AA:
Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 2.3e-90;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNRYGTMSTKNGITCOKWSTSPHRPRFSPATHPSGLEENYCRNP 60
Db 1 VYLSECKTGNGKNRYGTMSTKNGITCOKWSTSPHRPRFSPATHPSGLEENYCRNP 60
QY 61 DPOGFWCYTTDPEKRYDYCDILECEECMHCSENYDGKISKTWGSLGCOAWDSOP 120
Db 61 DPOGFWCYTTDPEKRYDYCDILECEECMHCSENYDGKISKTWGSLGCOAWDSOP 120
QY 121 GYIPSKRPKNOLKKNYCRNPDRILPWCFTTDPNKRWELCDIPRCTTTPSSGGTYO 180
Db 121 GYIPSKRPKNOLKKNYCRNPDRILPWCFTTDPNKRWELCDIPRCTTTPSSGGTYO 180
QY 181 GTEENYRGNVAVYSGHTCOHWSAQTHTERTPENPCNLDENYCRNPDGRAPCHT 240
Db 181 GTEENYRGNVAVYSGHTCOHWSAQTHTERTPENPCNLDENYCRNPDGRAPCHT 240
QY 241 TNSQVREWEYCKIPSCDSSPV 260
Db 241 TNSQVREWEYCKIPSCDSSPV 260
RESULT 10
ID AAW94038 standard; protein; 339 AA.
XX AAW94038;
XX AC
XX XX
DT 06-APR-1999 (first entry)

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XX XX Human angiotastatin fragment.
XX DE
XX XX
XX KM plasminogen; kringle; endothelial; angiogenesis; tumour; leukaemia;
XX KM rheumatoid arthritis; psoriasis; ocular angiogenic disease; ulcer;
XX KM gene therapy; birth control; Crohn's disease; angiotastatin.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key
XX FT Location/Qualifiers
XX FT Peptide
XX FT 6..255
XX FT /note= "Kringle 1-3"
XX FT Peptide
XX FT 6..165
XX FT /note= "Kringle 1-2"
XX FT Peptide
XX FT 6..84
XX FT /note= "Kringle 1"
XX FT Peptide
XX FT 88..255
XX FT /note= "Kringle 2-3"
XX FT Peptide
XX FT 88..165
XX FT /note= "Kringle 2"
XX FT Peptide
XX FT 178..255
XX FT /note= "Kringle 3"
XX XX
XX XX WO9854217-A1.
XX PN
XX XX 03-DEC-1998.
XX PD
XX XX
XX PF 29-MAY-1998; 98WO-US010979.
XX XX
XX PR 30-MAY-1997; 97US-00866735.
XX XX
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Folkman MJ, O'Reilly MS;
XX XX
XX XX WPI; 1999-059809/05.
XX DR
XX XX
XX PT Use of plasminogen fragments - having an amino acid sequence similar to
XX PT the kringle 1-5 region, for inhibiting endothelial cell proliferation and
XX PT angiogenesis.
XX PS
XX PS Example 27; Fig 2A-C; 165pp; English.
XX XX
XX CC The invention relates to inhibition of endothelial cell proliferation
XX CC that comprises administering to an endothelial cell a plasminogen
XX CC fragment having an amino acid sequence similar to the kringle 1-5 region
XX CC of a plasminogen molecule. The plasminogen fragments can be derived from
XX CC murine, human, Rhesus, porcine or bovine plasminogens. The plasminogen
XX CC fragments can be used for modulating angiogenesis and treating angiogenic
XX CC mediated disease e.g. solid tumours; for treating excessive or abnormal
XX CC stimulation of endothelial cells; as a birth control agent; and in the
XX CC treatment of diseases that have angiogenesis as a pathological
XX CC consequence (see AAW94036 for details on the various diseases the
XX CC plasminogen (see AAW94036 for details on the various diseases the
XX CC encoding the plasminogen fragments can also be used for gene therapy. The
XX CC products can be used for the production of antibodies and in detection
XX CC and diagnosis. Sequences AAW94037 to W4041 represent angiotastatin
XX CC fragments (protein derivatives of angiotastatin or plasminogen, having an
XX CC endothelial cell proliferation activity) of murine, human, Rhesus,
XX CC porcine and bovine angiotastatin respectively. The kringle regions that
XX CC can be used in the invention are indicated in the features
XX SQ
XX Sequence 339 AA:
Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 2.3e-90;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNRYGTMSTKNGITCOKWSTSPHRPRFSPATHPSGLEENYCRNP 60
Db 1 VYLSECKTGNGKNRYGTMSTKNGITCOKWSTSPHRPRFSPATHPSGLEENYCRNP 60
QY 61 DPOGFWCYTTDPEKRYDYCDILECEECMHCSENYDGKISKTWGSLGCOAWDSOP 120

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DB 61 DPGPMCTTDPKRYDYCDILCEBECCHSCGSENDGKISKMTSGLEQAMWSOPH 120
QY 121 GYIPSKFPNKLKKNYCRNPDRRLRPMWCTTDPNKMWELCDIPRCTTPSSSGPTVQCL 180
DB 121 GYIPSKFPNKLKKNYCRNPDRRLRPMWCTTDPNKMWELCDIPRCTTPSSSGPTVQCL 180
QY 181 GTGENTRGNAVAVTSGHTCOHMSAOTPHHTERTPENPCNDENYCRNPDGRAPWCHT 240
DB 181 GTGENTRGNAVAVTSGHTCOHMSAOTPHHTERTPENPCNDENYCRNPDGRAPWCHT 240
QY 241 TNSQVRMEYCKIIPSCDSSPV 260
DB 241 TNSQVRMEYCKIIPSCDSSPV 260

RESULT 11
AAMS0518
ID AAMS0518 standard; protein; 339 AA.
AC AAMS0518;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human angiotatin.
XX
KW Angiotatin; plasminogen; human; angiogenesis; endothelial cell;
KW cell proliferation; inhibitor; tumour; antiproliferative; cytostatic;
KW vasoregulator; antitumour; dermatological; antiinflammatory; antidiabetic;
KW antithrombotic; antiatherosclerotic; ophthalmological; vulnary; antidiabetic;
KW antibacterial; antiatherosclerotic; gynaecological; antipretic;
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 6..255
FT /label= Kringle-1-3
FT /label= 165
FT /label= Kringle-1-2
FT Region 6..84
FT /label= Kringle-1
FT /label= 255
FT Region 88..165
FT /label= Kringle-2-3
FT /label= 178
FT /label= 255
FT Region /label= Kringle-3
XX
PN US2001029246-A1.
XX
PD 11-OCT-2001.
XX
PF 16-FEB-2001; 2001US-00788142.
XX
PR 30-MAY-1997; 97US-00866735.
PR 24-APR-1998; 98US-00866028.
PR 11-MAY-1999; 99US-00309821.
PR 22-JUN-1999; 99US-00338387.
XX
PA (OREI/) O'REILLY M S.
PA (FOLK/) FOLKMAN M J.
PA (CAOY/) CAO Y.
XX
PI O'reilly MS, Folkman MJ, Cao Y;
XX
DR WPI; 2001-647990/74.
XX
PT Inhibiting endothelial cell proliferation, useful for treating angiogenic
PT mediated diseases such as cancer, arthritis, comprises administering
PT plasminogen fragment corresponding to kringle structures of plasminogen
PT molecule.
XX

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PS Example 27; Fig 2A-C; 70pp; English.
XX
CC The present sequence is that of human angiotatin. A claimed method of
CC inhibiting endothelial cell proliferation involves administering a
CC plasminogen fragment (PF) having an amino acid sequence similar to the
CC kringle 1-5 region of a plasminogen molecule. This includes a protein,
CC termed angiotatin, defined by its ability to overcome the angiogenic
CC activity of endogenous growth factors and by its amino acid sequence
CC homology and structural similarity to an internal portion of plasminogen,
CC beginning at approximately amino acid 98. The PF is preferably derived
CC from mouse, human, Rhesus monkey, pig or cattle (see AAMS0516-21). It is
CC used in methods and compositions for the treatment of an angiogenic-
CC mediated disease, including haemangioma, solid tumours, blood-borne
CC tumours, leukaemia, metastasis, telangiectasia, psoriasis,
CC atherosclerosis, scleroderma, pyogenic granuloma, myocardial
CC angiogenesis, Crohn's disease, plaque neovascularisation, coronary
CC collateral, cerebral collateral, arteriovenous malformations, ischaemic
CC limb angiogenesis, corneal diseases, rubeosis, neovascular glaucoma,
CC diabetic retinopathy, corneal graft rejection, retrolental fibroplasia,
CC haemophilic joints, rheumatoid arthritis, diabetic neovascularisation,
CC Osler-Webber syndrome, macular degeneration, wound healing, peptic ulcer,
CC Helicobacter pylori related diseases, fractures, keloids, vasculogenesis,
CC haematopoiesis, ovulation, menstruation, placentation and cat scratch
CC fever. Angiotatin is also useful as a birth control agent by preventing
CC vascularisation required for embryo implantation. The compositions are
CC particularly useful for treating or repressing the growth of tumours.
CC Administration of angiotatin to a human or animal with prevascularised
CC metastasised tumours will prevent the growth or expansion of those
CC tumours. Gene therapy methods are also included in the invention
XX
SQ Sequence 339 AA;

```

Query Match 99.7%; Score 1535; DB 4; Length 339;  
Best Local Similarity 99.6%; Pred. No. 2.3e-90;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 VYLSSECTGNGKNGYRGMTKNGITGQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
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DB 121 GYIPSKFPNKLKKNYCRNPDRRLRPMWCTTDPNKMWELCDIPRCTTPSSSGPTVQCL 180
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QY 241 TNSQVRMEYCKIIPSCDSSPV 260
DB 241 TNSQVRMEYCKIIPSCDSSPV 260

RESULT 12
ADG47024
ID ADG47024 standard; protein; 339 AA.
XX
AC ADG47024;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human angiotatin protein.
XX
KW Angiotatin; cell proliferation; angiogenic-mediated disease; cancer;
KW arthritis; macular degeneration; diabetic retinopathy; psoriasis;
KW scleroderma; Crohn's disease; wounds; peptic ulcer; fracture;
KW gene therapy; plasminogen; cytostatic; ophthalmological; dermatological;
KW antiinflammatory; vulnary; human.
XX

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Db 1 VYLSECKTGNGKNYRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPND 60  
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 Db 121 GYIPSKFPNNKLNKKNYCRNPDRRLRPMCFCTTDPKRWELCDIPRCTPPSSGPTYOCLK 180  
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 Db 181 GTGENYRGNAVAVTVSGHTCQWMSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240  
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 RESULT 14  
 AAY70255  
 ID AAY70255 standard; protein, 363 AA.  
 AC AAY70255;  
 XX  
 DT 06-JUN-2000 (first entry)  
 XX  
 DE Human angiogenesis inhibitor, angiostratin.  
 KW Human; immunoglobulin gamma Fc fragment; angiostratin; immunofusin;  
 KW angiogenesis; inhibitor; cycostatic; antirheumatoid; antiarthritic;  
 KW antidiabetic; ophthalmological; immunosuppressant;  
 KW vasotropic; vulvular; treatment; antiarteriosclerosis; tumour;  
 KW metastasis; atherosclerosis; psoriasis; rheumatoid arthritis;  
 KW ocular angiogenic disease; diabetic retinopathy; macular degeneration;  
 KW myocardial angiogenesis; plaque neovascularization; telangiectasia;  
 KW wound granulation; keloid scar; gene therapy.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200011033-A2.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 25-AUG-1999; 99WO-US019329.  
 XX  
 PR 25-AUG-1998; 98US-0097883P.  
 XX  
 PA (LEXI-) LEXINGEN PHARM CORP.  
 XX  
 PI Lo K, Li Y, Gillies SD;  
 XX  
 DR WPI; 2000-237616/20.  
 DR N-PSDB; AA251295.  
 XX  
 PT Novel fusion protein of angiostratin or endostatin and an immunoglobulin  
 PT FC region, useful for treating conditions mediated by angiogenesis, such  
 PT as rheumatoid arthritis, tumors and macular degeneration.  
 XX  
 PS Example 4; Page 45-46; 68pp; English.  
 CC The patent discloses a DNA molecule encoding a fusion protein comprising  
 CC a signal sequence, an immunoglobulin Fc region, and an angiogenesis  
 CC inhibitor selected from angiostratin, endostatin, a plasminogen fragment  
 CC having angiostratin activity, a collagen XVIII fragment having endostatin  
 CC activity, or combinations of them. The fusion protein (immunofusin) is  
 CC used to inhibit angiogenesis and to treat diseases or conditions mediated  
 CC by angiogenesis. Conditions that may be treated include solid tumours,  
 CC blood born tumours, tumour metastasis, benign tumours including  
 CC haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic  
 CC granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases  
 CC e.g. diabetic retinopathy, retinopathy of prematurity, macular  
 CC degeneration, corneal graft rejection, neovascular glaucoma, retrolental

CC fibroplasia, rubecosis and Osler-Webber syndrome; myocardial angiogenesis,  
 CC plaque neovascularization, telangiectasia, haemophilic joints,  
 CC angiofibroma, wound granulation, and excessive or abnormal stimulation of  
 CC endothelial cells, intestinal cells, atherosclerosis, sclerodermal and  
 CC hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in  
 CC gene therapy. The present sequence is a human angiostratin used in the  
 CC construction of immunofusin containing human immunoglobulin gamma (IgG)  
 CC Fc fragment  
 XX  
 SQ Sequence 363 AA;  
 Query Match 99.7%; Score 1535; DB 3; Length 363;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-90;  
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 Db 242 TNSQVRWEYCKIPSCDSSPV 261  
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 AAY02106  
 ID AAY02106 standard; protein, 364 AA.  
 AC AAY02106;  
 XX  
 DT 16-JUL-1999 (first entry)  
 XX  
 DE A multifunctional protein of the invention.  
 KW Angiostratin; endostatin; interferon; thrombospondin;  
 KW interferon-inducible protein; platelet factor 4; anti-angiogenic;  
 KW anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer;  
 KW diabetic retinopathy; macular degeneration; arthritis;  
 KW tumor cell production.  
 KW  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9916889-A1.  
 XX  
 PD 08-APR-1999.  
 XX  
 PF 30-SEP-1998; 98WO-US020464.  
 XX  
 PR 01-OCT-1997; 97US-0060609P.  
 XX  
 PA (SEAR) SEARLE & CO G D.  
 XX  
 PI Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK,  
 PI McKeown JP;  
 XX  
 DR WPI; 1999-255098/21.  
 XX  
 PT New multifunctional proteins useful for treating angiogenic-mediated  
 PT diseases.  
 XX

PS Claim 5; Page 101-102; 121pp; English.

XX The specification describes multifunctional proteins which comprise  
CC combinations of angiotensin, endostatin, interferon, thrombospondin,  
CC interferon-inducible protein and platelet factor 4, and have anti-  
CC angiogenic and/or anti-tumor activity. The multifunctional protein may  
CC exhibit useful properties such as having similar or greater biological  
CC activity when compared to a single factor or by having improved half-life  
CC or decreased adverse side effects, or a combination of these properties.  
CC The proteins can be used for treating an angiogenic-mediated disease,  
CC e.g., cancer, diabetic retinopathy, macular degeneration, or arthritis.  
CC They can also be used for inhibiting the production of tumor cells  
CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,  
CC colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)  
CC in a patient and for inhibiting tumor growth. The present sequence  
CC represents a multifunctional protein of the invention

XX Sequence 364 AA;

Query Match 99.7%; Score 1535; DB 2; Length 364;

Best Local Similarity 99.6%; Pred. No. 2.5e-90;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	121	GYIPSKFPNNKLLKKNYCRNPDRELPMCFITDPNKRWELCDIPRCTPPPSGPTYQCLK	180
DB	123	GYIPSKFPNNKLLKKNYCRNPDRELPMCFITDPNKRWELCDIPRCTPPPSGPTYQCLK	182
QY	181	GTGENYKGNNAVITSGHTCOHWSAQTPHTHERTEPENPCXKLDENYCRNPDGKRAPWCHT	240
DB	183	GTGENYKGNNAVITSGHTCOHWSAQTPHTNRTPENPCXKLDENYCRNPDGKRAPWCHT	242
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Job time : 75 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 27, 2005, 03:30:16; Search time 157 Seconds

(without alignments)  
644.191 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VILSECKTNGKNGKRYGTMSK.....TNSQVWEYCKIIPSCDSSEV 260

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched:

1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications, AA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1540	100.0	260	US-10-131-241-61	Sequence 61, Appl
2	1535	99.7	303	US-10-810-262-11	Sequence 11, Appl
3	1535	99.7	339	US-09-788-142-3	Sequence 3, Appl
4	1535	99.7	339	US-09-761-120-3	Sequence 3, Appl
5	1535	99.7	339	US-09-335-325-3	Sequence 3, Appl
6	1535	99.7	339	US-10-131-241-3	Sequence 3, Appl
7	1535	99.7	339	US-10-127-066-3	Sequence 3, Appl
8	1535	99.7	339	US-10-402-364-3	Sequence 3, Appl
9	1535	99.7	339	US-10-401-108-3	Sequence 3, Appl
10	1535	99.7	363	US-10-292-418-11	Sequence 11, Appl
11	1535	99.7	378	US-09-873-676-1	Sequence 1, Appl

12	1535	99.7	378	US-09-335-325-42	Sequence 42, Appl
13	1535	99.7	378	US-10-131-241-42	Sequence 42, Appl
14	1535	99.7	378	US-10-127-066-42	Sequence 42, Appl
15	1535	99.7	391	US-10-304-287-7	Sequence 7, Appl
16	1535	99.7	391	US-10-415-012-1	Sequence 1, Appl
17	1535	99.7	391	US-10-735-577-7	Sequence 7, Appl
18	1535	99.7	394	US-10-304-287-8	Sequence 8, Appl
19	1535	99.7	394	US-10-415-012-2	Sequence 2, Appl
20	1535	99.7	394	US-10-735-577-8	Sequence 8, Appl
21	1535	99.7	484	US-10-741-601-413	Sequence 413, App
22	1535	99.7	569	US-09-946-893-5	Sequence 5, Appl
23	1535	99.7	571	US-09-946-893-8	Sequence 8, Appl
24	1535	99.7	576	US-09-946-893-6	Sequence 6, Appl
25	1535	99.7	579	US-10-449-609-7	Sequence 7, Appl
26	1535	99.7	714	US-10-415-012-8	Sequence 8, Appl
27	1535	99.7	714	US-10-503-910-18	Sequence 18, Appl
28	1535	99.7	791	US-09-967-386-1	Sequence 1, Appl
29	1535	99.7	791	US-10-304-287-1	Sequence 1, Appl
30	1535	99.7	791	US-10-360-101-257	Sequence 257, App
31	1535	99.7	791	US-10-778-423-1	Sequence 1, Appl
32	1535	99.7	791	US-10-753-646-1	Sequence 1, Appl
33	1535	99.7	791	US-10-725-577-1	Sequence 1, Appl
34	1535	99.7	791	US-10-729-475-10	Sequence 10, Appl
35	1535	99.7	791	US-10-503-910-17	Sequence 17, Appl
36	1535	99.7	799	US-10-503-910-8	Sequence 8, Appl
37	1535	99.7	803	US-10-503-910-10	Sequence 10, Appl
38	1535	99.7	810	US-10-193-656-2	Sequence 2, Appl
39	1535	99.7	810	US-10-237-144-1	Sequence 1, Appl
40	1535	99.7	810	US-10-135-8728-4	Sequence 4, Appl
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42	1535	99.7	810	US-10-415-012-4	Sequence 4, Appl
43	1535	99.7	810	US-10-741-601-409	Sequence 409, App
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#### ALIGNMENTS

RESULT 1  
US-10-131-241-61  
Sequence 61, Application US/10131241  
Publication No. US20030012725A1  
GENERAL INFORMATION:  
APPLICANT: Holaday, John W.  
APPLICANT: Fortier, Anne H.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation  
FILE REFERENCE: 05213-0344 43170-271565  
CURRENT APPLICATION NUMBER: US/10/131,241  
PRIOR FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: US 09/413,049  
PRIOR FILING DATE: 1999-10-06  
PRIOR APPLICATION NUMBER: US 09/316,802  
PRIOR FILING DATE: 1999-05-21  
PRIOR APPLICATION NUMBER: US 60/086,586  
PRIOR FILING DATE: 1998-05-22  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 61  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-131-241-61  
Query Match 100.0%; Score 1540; DB 14; Length 260;  
Best Local Similarity 100.0%; Pred. No. 2e-120;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 2  
US-10-810-262-11  
Sequence 11, Application US/10810262  
Publication No. US20040234505A1  
GENERAL INFORMATION:  
APPLICANT: NAVILOR, STUART  
APPLICANT: KINGSMAN, SUSAN MARY  
APPLICANT: BINLEY, KATIE  
TITLE OF INVENTION: POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF  
FILE REFERENCE: 674523-2029-1  
CURRENT APPLICATION NUMBER: US/10/810, 262  
CURRENT FILING DATE: 2004-03-26  
PRIOR APPLICATION NUMBER: 09/787, 562  
PRIOR FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: PCT/GB99/03181  
PRIOR FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: PCT/GB98/02885  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: GB 9901906.9  
PRIOR FILING DATE: 1999-01-28  
PRIOR APPLICATION NUMBER: GB 9903538.8  
PRIOR FILING DATE: 1999-02-16  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 11  
LENGTH: 303  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-810-262-11

Query Match 99.7%; Score 1535; DB 16; Length 303;  
Best Local Similarity 99.6%; Pred. No. 6.1e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 3

US-09-788-142-3  
Sequence 3, Application US/09788142  
Patent No. US20010029246A1  
GENERAL INFORMATION:  
APPLICANT: Folkmann, M. Judah  
O'Reilly, Michael  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 09/788,142  
FILING DATE: 16-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/866,735  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05940-0129  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 818-3700  
TELEFAX: (404) 818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-788-142-3  
Query Match 99.7%; Score 1535; DB 9; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6.9e-120;  
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Db 61 DPGWCYTTDPKRYDYCDILCEBECMHCSENGYDGIKSTMSGLECAMDSQSPH 120  
Qy 121 GYISKFPKNKLNKKNYCNPNRPRPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCL 180  
Db 121 GYISKFPKNKLNKKNYCNPNRPRPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCL 180  
Qy 181 GTGENYRGNVAVTYSGHTCOHMSAOTPHRTHERTPENPCKNLDENYCRNPDGRAPWCHT 240  
Db 181 GTGENYRGNVAVTYSGHTCOHMSAOTPHRTHERTPENPCKNLDENYCRNPDGRAPWCHT 240  
Qy 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

Db 241 TNSOVRMEYCKIPSCDSSPV 260

RESULT 4  
US-09-761-120-3  
Sequence 3, Application US/09761120  
Patent No. US20020037847A1  
GENERAL INFORMATION:  
APPLICANT: O'Reilly, M. Judah  
APPLICANT: Folkmann, Michael  
TITLE OF INVENTION: Nucleic Acids Encoding Kriingle 1-5 Region Fragments of Plasminogen  
FILE REFERENCE: 05940-0151 (43171-252068)  
CURRENT APPLICATION NUMBER: US/09/761,120  
CURRENT FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 09/309,821  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 08/866,735  
PRIOR FILING DATE: 1997-05-30  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: Patentin version 3.0  
SEQ ID NO: 339  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-761-120-3

Query Match 99.7%; Score 1535; DB 9; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6.9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGTMKTKNGITCQKMSSTSPHPRPSRPAHPSEGLSENYCRPN 60  
Db 1 VYLSECKTGNGKNGYRGTMKTKNGITCQKMSSTSPHPRPSRPAHPSEGLSENYCRPN 60  
QY 61 DPQGPWCYTTDPKRYDYCDILECEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAH 120  
Db 61 DPQGPWCYTTDPKRYDYCDILECEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAH 120  
QY 121 GIYPSKFPNKNLKNYCRNPDRRLPWCFTTDPNKRWEICDIPRCTTTPSSGPTYQCLK 180  
Db 121 GIYPSKFPNKNLKNYCRNPDRRLPWCFTTDPNKRWEICDIPRCTTTPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPHTHERTPENPCXNLDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENYRGNAVAVTSGHTCOHWSAQTPHTHERTPENPCXNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSOVRMEYCKIPSCDSSPV 260  
Db 241 TNSOVRMEYCKIPSCDSSPV 260

RESULT 5  
US-09-335-325-3  
Sequence 3, Application US/09335325  
Patent No. US20020164717A1  
GENERAL INFORMATION:  
APPLICANT: Folkmann, M. Judah  
APPLICANT: O'Reilly, Michael  
APPLICANT: Cao, Yihai  
APPLICANT: Sim, B. Kim Lee

TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESS: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/335,325  
FILING DATE: 17-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Marten, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-335-325-3

Query Match 99.7%; Score 1535; DB 9; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6.9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGTMKTKNGITCQKMSSTSPHPRPSRPAHPSEGLSENYCRPN 60  
Db 1 VYLSECKTGNGKNGYRGTMKTKNGITCQKMSSTSPHPRPSRPAHPSEGLSENYCRPN 60  
QY 61 DPQGPWCYTTDPKRYDYCDILECEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAH 120  
Db 61 DPQGPWCYTTDPKRYDYCDILECEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAH 120  
QY 121 GIYPSKFPNKNLKNYCRNPDRRLPWCFTTDPNKRWEICDIPRCTTTPSSGPTYQCLK 180  
Db 121 GIYPSKFPNKNLKNYCRNPDRRLPWCFTTDPNKRWEICDIPRCTTTPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPHTHERTPENPCXNLDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENYRGNAVAVTSGHTCOHWSAQTPHTHERTPENPCXNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSOVRMEYCKIPSCDSSPV 260  
Db 241 TNSOVRMEYCKIPSCDSSPV 260

RESULT 6  
US-10-131-241-3  
Sequence 3, Application US/10131241  
Publication No. US20030012792A1  
GENERAL INFORMATION:  
APPLICANT: Holaday, John W.  
APPLICANT: Fortier, Anne H.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation  
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers  
FILE REFERENCE: 05213-0344 43170-271565  
CURRENT APPLICATION NUMBER: US/10/131,241  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: US 09/413,049  
PRIOR FILING DATE: 1999-10-06  
PRIOR APPLICATION NUMBER: US 09/316,802  
PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: US 60/086,586  
PRIOR FILING DATE: 1998-05-22  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-131-241-3

Query Match 99.7%; Score 1535; DB 14; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6,9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGKRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGKRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPOGWCYTTDPEKRYDYCDILECEECHMGSGENYDGIKSTKMSGLECOAMDSOPHAAH 120  
DB 61 DPOGWCYTTDPEKRYDYCDILECEECHMGSGENYDGIKSTKMSGLECOAMDSOPHAAH 120  
QY 121 GIYPSKFPKNNLKKNYCRNPDELRLPWCFTTDPNKKWELCDIPRCTPPSSSGPTYQCLK 180  
DB 121 GIYPSKFPKNNLKKNYCRNPDELRLPWCFTTDPNKKWELCDIPRCTPPSSSGPTYQCLK 180  
QY 181 GTGENYRGNAVATVSGHTCOHWSAOTPHHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVATVSGHTCOHWSAOTPHHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 7  
US-10-127-066-3  
Sequence 3, Application US/10127066  
Publication No. US20030064926A1  
GENERAL INFORMATION:  
APPLICANT: O'Reilly, Michael S.  
APPLICANT: Folkman, M. Judah  
APPLICANT: Cao, Yihai  
APPLICANT: Sim, Kim Lee  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
FILE REFERENCE: 05213-0612 43170-272529  
CURRENT APPLICATION NUMBER: US/10/127,066  
CURRENT FILING DATE: 2002-07-23  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-127-066-3

Query Match 99.7%; Score 1535; DB 14; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6,9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGKRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGKRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPOGWCYTTDPEKRYDYCDILECEECHMGSGENYDGIKSTKMSGLECOAMDSOPHAAH 120  
DB 61 DPOGWCYTTDPEKRYDYCDILECEECHMGSGENYDGIKSTKMSGLECOAMDSOPHAAH 120  
QY 121 GIYPSKFPKNNLKKNYCRNPDELRLPWCFTTDPNKKWELCDIPRCTPPSSSGPTYQCLK 180  
DB 121 GIYPSKFPKNNLKKNYCRNPDELRLPWCFTTDPNKKWELCDIPRCTPPSSSGPTYQCLK 180  
QY 181 GTGENYRGNAVATVSGHTCOHWSAOTPHHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240

DB 181 GTGENYRGNAVATVSGHTCOHWSAOTPHHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 8  
US-10-402-364-3  
Sequence 3, Application US/10402364  
Publication No. US20040002459A1  
GENERAL INFORMATION:  
APPLICANT: O'Reilly, Michael  
APPLICANT: Folkman, M. Judah  
TITLE OF INVENTION: Nucleic Acids Encoding Kringles 1-5 Region Fragments of Plasminogen  
FILE REFERENCE: 05213-2151 (43170-252068)  
CURRENT APPLICATION NUMBER: US/10/402,364  
CURRENT FILING DATE: 2003-03-28  
PRIOR APPLICATION NUMBER: US/09/761,120A  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 09/309,821  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 08/866,735  
PRIOR FILING DATE: 1997-05-30  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-402-364-3

Query Match 99.7%; Score 1535; DB 15; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6,9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGKRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGKRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPOGWCYTTDPEKRYDYCDILECEECHMGSGENYDGIKSTKMSGLECOAMDSOPHAAH 120  
DB 61 DPOGWCYTTDPEKRYDYCDILECEECHMGSGENYDGIKSTKMSGLECOAMDSOPHAAH 120  
QY 121 GIYPSKFPKNNLKKNYCRNPDELRLPWCFTTDPNKKWELCDIPRCTPPSSSGPTYQCLK 180  
DB 121 GIYPSKFPKNNLKKNYCRNPDELRLPWCFTTDPNKKWELCDIPRCTPPSSSGPTYQCLK 180  
QY 181 GTGENYRGNAVATVSGHTCOHWSAOTPHHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVATVSGHTCOHWSAOTPHHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 9  
US-10-401-108-3  
Sequence 3, Application US/10401108  
Publication No. US20040023877A1  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
APPLICANT: O'Reilly, Michael  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA

ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/401,108  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/866,735  
FILING DATE: 30-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05940-0129  
TELEPHONE: (404) 818-3700  
TELEFAX: (404) 818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiotensin fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-401-108-3

Query Match 99.7%; Score 1535; DB 15; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6.9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 VYLSECKTGNGKNGYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPN 60  
1 VILSECKTGNGKNGYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPN 60  
61 DPGPWCYTTDPKRYDYCDILECEBECMHSGENYDGIKSTMSGLECOAMDOSPHAH 120  
61 DPGPWCYTTDPKRYDYCDILECEBECMHSGENYDGIKSTMSGLECOAMDOSPHAH 120  
121 GYIPSKFPMKLNKKNYCRNPRELRPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCLK 180  
121 GYIPSKFPMKLNKKNYCRNPRELRPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCLK 180  
121 GYIPSKFPMKLNKKNYCRNPRELRPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCLK 180  
181 GGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCKNIDENYCRNPDGRAPWCHT 240  
181 GGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCKNIDENYCRNPDGRAPWCHT 240  
181 GGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCKNIDENYCRNPDGRAPWCHT 240  
241 TNSQVMEYCKIIPSCDSSPV 260  
241 TNSQVMEYCKIIPSCDSSPV 260  
241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 10  
US-10-292-418-11  
Sequence 11, Application US/10292418  
Publication No. US20030139365A1  
GENERAL INFORMATION:  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Li, Yue  
APPLICANT: Gillies, Stephen D  
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as  
TITLE OF INVENTION: Immunofusins  
FILE REFERENCE: LEX-006C1

CURRENT APPLICATION NUMBER: US/10/292,418  
CURRENT FILING DATE: 2002-11-12  
PRIOR APPLICATION NUMBER: 09/383,315  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: US 60/097,883  
PRIOR FILING DATE: 1998-06-25  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 11  
LENGTH: 363  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-292-418-11

Query Match 99.7%; Score 1535; DB 14; Length 363;  
Best Local Similarity 99.6%; Pred. No. 7.5e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 VYLSECKTGNGKNGYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPN 60  
2 VYLSECKTGNGKNGYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPN 61  
61 DPGPWCYTTDPKRYDYCDILECEBECMHSGENYDGIKSTMSGLECOAMDOSPHAH 120  
62 DPGPWCYTTDPKRYDYCDILECEBECMHSGENYDGIKSTMSGLECOAMDOSPHAH 121  
121 GYIPSKFPMKLNKKNYCRNPRELRPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCLK 180  
122 GYIPSKFPMKLNKKNYCRNPRELRPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCLK 181  
181 GGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCKNIDENYCRNPDGRAPWCHT 240  
182 GGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCKNIDENYCRNPDGRAPWCHT 241  
241 TNSQVMEYCKIIPSCDSSPV 260  
242 TNSQVMEYCKIIPSCDSSPV 261

RESULT 11  
US-09-873-676-1  
Sequence 1, Application US/09873676  
Patent No. US20020077289A1  
GENERAL INFORMATION:  
APPLICANT: Macdonald, Nicholas J.  
APPLICANT: Sim, Kim L.  
TITLE OF INVENTION: Angiotensin and Endostatin Binding Proteins and Methods of Use  
FILE REFERENCE: 05213-0378 (43170-259333)  
CURRENT FILING DATE: US/09/873,676  
PRIOR APPLICATION NUMBER: 2001-06-04  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US 60/209,065  
PRIOR FILING DATE: 2001-05-08  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: Patent version 3.1  
SEQ ID NO 1  
LENGTH: 378  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-873-676-1

Query Match 99.7%; Score 1535; DB 9; Length 378;  
Best Local Similarity 99.6%; Pred. No. 7.8e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 VYLSECKTGNGKNGYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPN 60  
6 VYLSECKTGNGKNGYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPN 65  
61 DPGPWCYTTDPKRYDYCDILECEBECMHSGENYDGIKSTMSGLECOAMDOSPHAH 120  
62 DPGPWCYTTDPKRYDYCDILECEBECMHSGENYDGIKSTMSGLECOAMDOSPHAH 125

QY 121 GYIPSKFPKXNKKYCRNPDLRPMWCTTDPNKRWELCDIPRCTPPSSGPTYOCLK 180  
DB 126 GYIPSKFPKXNKKYCRNPDLRPMWCTTDPNKRWELCDIPRCTPPSSGPTYOCLK 185  
QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGKRAFWCHT 240  
DB 186 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGKRAFWCHT 245  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 246 TNSQVRWEYCKIPSCDSSPV 265

RESULT 12  
US-09-335-325-42  
Sequence 42, Application US/093335325  
Patent No. US20020164717A1  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
O'Reilly, Michael  
Cao, Yihai  
Sim, B. Kim Lee  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/335,325  
FILING DATE: 17-Jun-1999  
CLASSIFICATION DATA:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 378 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: K1-4BKLS  
SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-09-335-325-42

Query Match 99.7%; Score 1535; DB 9; Length 378;  
Best Local Similarity 99.6%; Pred. No. 7.8e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 VYLSECKTNGKXNYRGTMSTKNGITCOKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60

DB 6 VYLSECKTNGKXNYRGTMSTKNGITCOKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 65  
QY 61 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGKISKTMSGLECOAMDSPHAF 120  
DB 66 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGKISKTMSGLECOAMDSPHAF 125  
QY 121 GYIPSKFPKXNKKYCRNPDLRPMWCTTDPNKRWELCDIPRCTPPSSGPTYOCLK 180  
DB 126 GYIPSKFPKXNKKYCRNPDLRPMWCTTDPNKRWELCDIPRCTPPSSGPTYOCLK 185  
QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGKRAFWCHT 240  
DB 186 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGKRAFWCHT 245  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 246 TNSQVRWEYCKIPSCDSSPV 265

RESULT 13  
US-10-131-241-42  
Sequence 42, Application US/10131241  
Publication No. US20030012792A1  
GENERAL INFORMATION:  
APPLICANT: Holaday, John W.  
Fortier, Anne H.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/131,241  
FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: US 09/413,049  
PRIOR FILING DATE: 1999-10-06  
PRIOR APPLICATION NUMBER: US 09/316,802  
PRIOR FILING DATE: 1999-05-21  
PRIOR APPLICATION NUMBER: US 60/086,586  
PRIOR FILING DATE: 1998-05-22  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 42  
LENGTH: 378  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-131-241-42

Query Match 99.7%; Score 1535; DB 14; Length 378;  
Best Local Similarity 99.6%; Pred. No. 7.8e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 VYLSECKTNGKXNYRGTMSTKNGITCOKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60  
DB 6 VYLSECKTNGKXNYRGTMSTKNGITCOKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 65  
QY 61 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGKISKTMSGLECOAMDSPHAF 120  
DB 66 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGKISKTMSGLECOAMDSPHAF 125  
QY 121 GYIPSKFPKXNKKYCRNPDLRPMWCTTDPNKRWELCDIPRCTPPSSGPTYOCLK 180  
DB 126 GYIPSKFPKXNKKYCRNPDLRPMWCTTDPNKRWELCDIPRCTPPSSGPTYOCLK 185  
QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGKRAFWCHT 240  
DB 186 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGKRAFWCHT 245  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 246 TNSQVRWEYCKIPSCDSSPV 265

RESULT 14  
US-10-127-066-42



Sequence 42: Application US/10127066  
Publication NO: US20030064926A1  
GENERAL INFORMATION:  
APPLICANT: O'Reilly, Michael S.  
APPLICANT: Folkman, M. Judah  
APPLICANT: Cao, Yihai  
APPLICANT: Sim, Kim Lee  
TITLE OF INVENTION: Angiotensin Fragments and Method of Use  
FILE REFERENCE: 05213-0612 43170-272529  
CURRENT APPLICATION NUMBER: US/10/127,066  
CURRENT FILING DATE: 2002-07-23  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 42  
LENGTH: 378  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-127-066-42

Query Match 99.7%; Score 1535; DB 14; Length 378;  
Best Local Similarity 99.6%; Pred. No. 7.8e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKRYRGTMSTKNGITCQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
DB 6 VYLSECKTGNGKRYRGTMSTKNGITCQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 65  
QY 61 DPOGPMCTTDPPEKRYDYCDILECEECMHGSGENYDGIKSTMSGLECOAMDOSPPAH 120  
DB 66 DPOGPMCTTDPPEKRYDYCDILECEECMHGSGENYDGIKSTMSGLECOAMDOSPPAH 125  
QY 121 GYIPSKFPNKKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180  
DB 126 GYIPSKFPNKKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 185  
QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPHTHERTPENPCKNLDENYCRNPDGRAPWCHT 240  
DB 186 GTGENYRGNAVAVTSGHTCOHMSAQTPHTHERTPENPCKNLDENYCRNPDGRAPWCHT 245  
QY 241 TNSQVRMEYCKIPSCDSSPV 260  
DB 246 TNSQVRMEYCKIPSCDSSPV 265

RESULT 15  
US-10-304-287-7  
Sequence 7: Application US/10304287  
Publication NO: US20030083234A1  
GENERAL INFORMATION:  
APPLICANT: Walsman, David M.  
APPLICANT: Kwon, Mijung  
TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor  
FILE REFERENCE: ME02-001  
CURRENT APPLICATION NUMBER: US/10/304,287  
CURRENT FILING DATE: 2002-11-26  
PRIOR APPLICATION NUMBER: US 60/333,866  
PRIOR FILING DATE: 2001-11-28  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Microsoft Word  
SEQ ID NO 7  
LENGTH: 391  
TYPE: PRT  
ORGANISM: mammalian  
US-10-304-287-7

Query Match 99.7%; Score 1535; DB 14; Length 391;  
Best Local Similarity 99.6%; Pred. No. 8.1e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKRYRGTMSTKNGITCQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
DB 2 VYLSECKTGNGKRYRGTMSTKNGITCQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 61

QY 61 DPOGPMCTTDPPEKRYDYCDILECEECMHGSGENYDGIKSTMSGLECOAMDOSPPAH 120  
DB 62 DPOGPMCTTDPPEKRYDYCDILECEECMHGSGENYDGIKSTMSGLECOAMDOSPPAH 121  
QY 121 GYIPSKFPNKKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180  
DB 122 GYIPSKFPNKKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 181  
QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPHTHERTPENPCKNLDENYCRNPDGRAPWCHT 240  
DB 182 GTGENYRGNAVAVTSGHTCOHMSAQTPHTHERTPENPCKNLDENYCRNPDGRAPWCHT 241  
QY 241 TNSQVRMEYCKIPSCDSSPV 260  
DB 242 TNSQVRMEYCKIPSCDSSPV 261

Search completed: July 27, 2005, 03:43:22  
Job time : 158 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 27, 2005, 03:24:10 ; Search time 16 seconds  
(without alignments)

1563.522 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGNGKRYRGTMK.....TNSQVWEYCKIPSCDSSPV 260

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:.\*  
1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1535	99.7	810	1	PLHU
2	1442	93.6	810	2	PLHU
3	1292	83.9	790	1	PLPG
4	1291	83.8	812	1	PLBO
5	1274	82.7	812	1	PLMS
6	1237	80.3	810	2	PLMS
7	881	57.2	2869	2	TI8518
8	797	51.8	728	1	UH0579
9	782	50.4	728	1	A35644
10	776.5	50.4	710	1	IS1283
11	776	50.4	728	1	A60185
12	766.5	49.8	716	1	JCS061
13	754.5	49.0	411	2	IS1285
14	753.5	48.9	716	1	A40332
15	749	48.6	4548	1	S00657
16	739	48.0	711	1	A47136
17	739	48.0	1420	2	A33869
18	505	32.8	455	2	A61545
19	499	32.4	460	2	B61545
20	391.5	25.4	336	2	B61545
21	372	24.2	625	2	TSBO
22	362.5	23.5	169	2	A40522
23	357.5	23.2	618	2	A35827
24	351	22.8	622	2	TSBU
25	348	22.6	617	2	SI0511
26	309.5	19.2	562	1	UKHUT
27	295.5	19.1	559	1	A35029
28	281.5	18.3	559	1	A29941
29	278	18.1	120	2	B61545

## ALIGNMENTS

30	271	17.6	89	2	A60140	plasma (EC 3.4.21
31	268	17.4	123	2	C61545	plasma (EC 3.4.21
32	241.5	15.7	937	2	A45082	neurotrophic recep
33	240	15.6	943	2	B45082	neurotrophic recep
34	237.5	15.4	946	1	A47299	cor-related recept
35	233	15.1	603	2	S28941	coagulation factor
36	214	13.9	558	2	JCS878	plasma hyaluronan
37	210	13.6	560	1	UC4795	plasma hyaluronan
38	201	13.1	291	2	I38098	t-plasminogen acti
39	198	12.9	615	1	KPHU12	coagulation factor
40	190.5	12.4	593	2	S45281	coagulation factor
41	188.5	12.2	655	1	A46688	hepatocyte growth
42	178.5	11.6	806	2	T18840	hypothetical prote
43	165	10.7	433	1	UN0560	u-plasminogen acti
44	153	9.9	442	1	UKRG	u-plasminogen acti
45	151	9.8	432	1	S18932	u-plasminogen acti

## RESULT 1

### PLHU

plasma (EC 3.4.21.7) precursor [validated] - human  
N:Alternate names: plasminogen precursor [misnomer]  
N:Contains: angiotensin, microplasmin, plasminogen  
C:Species: Homo sapiens (man)  
C:Dates: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 09-Jul-2004  
C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A0-  
R:Peterson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, B.W.  
J. Biol. Chem. 265: 6104-6111, 1990  
A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolysis  
A:Reference number: A35229; MUID:90202879; PMID:2318848  
A:Accession: A35229  
A:Molecule type: DNA  
A:Residues: 1-810 <PRT>  
A:Cross-references: UNIPROT:P00747; UNIPROT:Q9UHQ9; UNIPROT:Q9UW12; GB:J05286; GB:M34276  
A:Experimental source: Leukocyte; lung fibroblast  
R:Malgaroli, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; T-  
Biochem. Biophys. Res. Commun. 173: 1013-1018, 1990  
A:Title: Definition of the transcription initiation site of human plasminogen gene in 15  
A:Reference number: I52242; MUID:91097523; PMID:2268308  
A:Accession: I52242  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-16 <MAL1>  
A:Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613  
R:Forstgen, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.  
FEBS Lett. 213: 254-260, 1987  
A:Title: Molecular cloning and characterization of a full-length cDNA clone for human p1  
A:Reference number: A26646; MUID:87162490; PMID:3030813  
A:Accession: A26646  
A:Molecule type: mRNA  
A:Residues: 1-471, 'D', 473-810 <FOR>  
A:Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531  
A:Experimental source: liver  
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.  
Biochemistry 23: 4243-4250, 1984  
A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and  
A:Reference number: I45961; MUID:95023311; PMID:6148961  
A:Accession: I62738  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 292-471, 'D', 473-810 <MAL2>  
A:Cross-references: GB:K02922; NID:g190112; PIDN:AAA60124.1; PID:g387031  
A:Accession: I84609  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 367-419 <MAL3>  
A:Cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:g190111  
R:Brundsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lejter, W.; Manneberg, M.;  
Eur. J. Biochem. 114: 465-470, 1981  
A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,

A:Reference number: S03735; MUID:81212097; PMID:7238497  
A:Accession: S03735  
A:Molecule type: protein  
A:Residues: 20-71, 'E', 73-76 <BRU>  
R:Sortrup-Jensen, L.; Petersen, T.E.; Magnusson, S.  
submitted to the Atlas, July 1977  
A:Reference number: A00929  
A:Accession: A00929  
A:Molecule type: protein  
A:Residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>  
R:Wiman, B.  
Eur. J. Biochem. 76, 129-137, 1977  
A:Title: Primary structure of the B-chain of human plasmin.  
A:Reference number: A04627; MUID:77225245; PMID:142009  
A:Accession: A04627  
A:Molecule type: protein  
A:Residues: 581-810 <WII>  
R:Wiman, B.; Wallen, P.  
Eur. J. Biochem. 50, 489-494, 1975  
A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen.  
A:Reference number: A04625; MUID:75093329; PMID:122932  
A:Accession: A04625  
A:Molecule type: protein  
A:Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <WII>  
R:Wiman, B.; Wallen, P.  
Eur. J. Biochem. 58, 539-547, 1975  
A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen that is homologous to the epsilon-chain of human fibrinogen.  
A:Reference number: A04626; MUID:76043692; PMID:126863  
A:Accession: A04626  
A:Molecule type: protein  
A:Residues: 483-507, 'E', 509-604 <WII>  
R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.  
J. Biol. Chem. 248, 1631-1633, 1973  
A:Title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen.  
A:Reference number: A92125; MUID:73149248; PMID:4694729  
A:Contents: annotation; active site  
J:Groskopf, W.R.; Summaria, L.; Robbins, K.C.  
J. Biol. Chem. 244, 3590-3597, 1969  
A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a fragment of human plasminogen.  
A:Reference number: A92048; MUID:69234739; PMID:4240117  
A:Contents: annotation; active site  
R:Trexler, M.; Vail, Z.; Parthy, L.  
J. Biol. Chem. 257, 7401-7406, 1982  
A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.  
A:Reference number: A92382; MUID:82213905; PMID:6919539  
A:Contents: annotation; omega-aminocarboxylic acid binding sites  
R:Vail, Z.; Parthy, L.  
J. Biol. Chem. 259, 13690-13694, 1984  
A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential for fibrin binding.  
A:Reference number: A92458; MUID:85054794; PMID:6094526  
A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site  
R:Guo, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Seehndel, S.; McCance, S.G.; et al.  
J. Biol. Chem. 271, 29461-29467, 1996  
A:Title: Kringel domains of human angiotensin. Characterization of the anti-proliferative activity of the anti-proliferative domain.  
A:Reference number: A58811; MUID:97067211; PMID:8910613  
A:Contents: annotation  
R:Li, H.; Hsu, H.; Uemura, F.; Bini, A.; Collen, D.  
Biochemistry 37, 4699-4702, 1998  
A:Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (MMP-3).  
A:Reference number: A58812; MUID:95487733; PMID:95487733  
A:Contents: annotation  
R:Tulinsky, A.; Mullach, A.M.  
submitted to the Brookhaven Protein Data Bank, July 1991  
A:Reference number: A51341; PDB:1IPK4  
A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454  
R:Tulinsky, A.; Wu, T.P.  
submitted to the Brookhaven Protein Data Bank, July 1991  
A:Reference number: A51488; PDB:2PK4  
A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454  
R:Mu, T.P.; Tulinsky, A.  
submitted to the Brookhaven Protein Data Bank, August 1993  
A:Reference number: A51911; PDB:1IPK8

[illegible]

F:79-466/Product: angiotensin #status experimental <ASN>  
 F:97-580,581-810/Product: plasmin #status experimental <MAT>  
 F:97-580/Domain: plasmin chain A #status experimental <CHA>  
 F:103-181/Domain: kringle homology <KR1>  
 F:185-262/Domain: kringle homology <KR2>  
 F:275-352/Domain: kringle homology <KR3>  
 F:377-454/Domain: kringle homology <KR4>  
 F:481-560/Domain: kringle homology <KR5>  
 F:550-580,581-810/Product: microplasmin #status experimental <MMT>

Query Match 99.7%; Score 1535; DB 1; Length 810;  
 Best Local Similarity 99.6%; Pred. No. 5,66-104;  
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECTGNGKNGKNGKNGITGCKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
 DB VYLSECTGNGKNGKNGKNGITGCKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 157  
 QY 61 DPGPMCYTTDPEKRYVYCDILECEBOMHSGENYCKISKTMSGLECAMDSOPHAA 120  
 DB DPGPMCYTTDPEKRYVYCDILECEBOMHSGENYCKISKTMSGLECAMDSOPHAA 217  
 QY 121 GYIPSKFPMKLNKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTPPSSGPTVQCLK 180  
 DB GYIPSKFPMKLNKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTPPSSGPTVQCLK 277  
 QY 218 GYIPSKFPMKLNKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTPPSSGPTVQCLK 277  
 DB 218 GYIPSKFPMKLNKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTPPSSGPTVQCLK 277  
 QY 181 GTGENTRGNAVAVTSGHTCQMSAQTPTHTERTPENPCNLDENYCRNPDGRAPWCHT 240  
 DB 278 GTGENTRGNAVAVTSGHTCQMSAQTPTHTERTPENPCNLDENYCRNPDGRAPWCHT 337  
 QY 241 TNSQVMEYCKIPSCSSPV 260  
 DB 338 TNSQVMEYCKIPSCSSPV 357

## RESULT 2

plasmin (EC 3.4.21.7) precursor - rhesus macaque  
 C/Species: Macaca mulatta (rhesus macaque)  
 C/Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
 C/Accession: B32869; B30848  
 R/Tomlinson, J.E.; McLean, J.W.; Lawm, R.M.  
 J. Biol. Chem. 264, 5957-5965, 1989  
 A>Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.  
 A/Reference number: A32869; MUID:89174660; PMID:2925643  
 A/Accession: B32869  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1810 <TOM>  
 A/Cross-references: UNIPROT:P12545; GB:004697; NID:G342272; PIDN:AAA36901.1; PID:G342273  
 C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology  
 C/Keywords: fibrinolysis; glycoprotein; hydrolyase; kringle; serine proteinase  
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>  
 F:1-9/Domain: signal sequence #status predicted <SIG>  
 F:103-181/Domain: kringle homology <KR1>  
 F:185-262/Domain: kringle homology <KR2>  
 F:275-352/Domain: kringle homology <KR3>  
 F:377-454/Domain: kringle homology <KR4>  
 F:481-560/Domain: kringle homology <KR5>  
 F:581-803/Domain: trypsin homology <TRY>  
 F:59-73,55-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32  
 bonds: #status predicted  
 F:622,665,760/Active site: His, Asp, Ser #status predicted

Query Match 93.6%; Score 1442; DB 2; Length 810;  
 Best Local Similarity 93.1%; Pred. No. 3,1e-97;  
 Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 VYLSECTGNGKNGKNGKNGITGCKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
 DB VYLSECTGNGKNGKNGKNGITGCKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 157  
 QY 61 DPGPMCYTTDPEKRYVYCDILECEBOMHSGENYCKISKTMSGLECAMDSOPHAA 120

DB 158 DPGPMCYTTDPEKRYVYCDILECEBOMHSGENYCKISKTMSGLECAMDSOPHAA 217  
 QY 121 GYIPSKFPMKLNKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTPPSSGPTVQCLK 180  
 DB 218 GYIPSKFPMKLNKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTPPSSGPTVQCLK 277  
 QY 181 GTGENTRGNAVAVTSGHTCQMSAQTPTHTERTPENPCNLDENYCRNPDGRAPWCHT 240  
 DB 278 GTGENTRGNAVAVTSGHTCQMSAQTPTHTERTPENPCNLDENYCRNPDGRAPWCHT 337  
 QY 241 TNSQVMEYCKIPSCSSPV 260  
 DB 338 TNSQVMEYCKIPSCSSPV 357

## RESULT 3

plasmin (EC 3.4.21.7) precursor - pig (fragment)  
 N/Alternate names: plasminogen  
 N/Contains: miniplasminogen  
 C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 07-Sep-1990 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
 C/Accession: S03733; S03737; A25834  
 R/Schaller, J.; Marti, T.; Roesseler, S.J.; Kaempfer, U.; Rickli, E.E.  
 Fibrinolysis 1, 91-102, 1987

A>Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the c  
 A/Reference number: S03735; MUID:81212097; PMID:7238497  
 A/Accession: S03733  
 A/Molecule type: protein  
 A/Residues: 1-560 <SCH>  
 A/Cross-references: UNIPROT:P06867  
 R/Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.  
 Eur. J. Biochem. 114, 465-470, 1981  
 A>Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,  
 A/Reference number: S03735; MUID:81212097; PMID:7238497  
 A/Accession: S03737  
 A/Molecule type: protein  
 A/Residues: 1-57 <BRU>  
 R/Marti, T.; Schaller, J.; Rickli, E.E.  
 Eur. J. Biochem. 149, 279-285, 1985

A>Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.  
 A/Reference number: A25834; MUID:85203907; PMID:3846533  
 A/Accession: A25834  
 A/Molecule type: protein  
 A/Residues: 450-790 <MAR>  
 C/Function: dissolves the fibrin of blood clots; acts as a proteolytic factor in a v  
 as the walls of the granafian follicle; also activates the urokinase-type plasminogen acti  
 A/Pathway: fibrinolysis  
 C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology  
 C/Keywords: fibrinolysis; glycoprotein; hydrolyase; kidney; kringle; plasma; serine prot  
 F:1-790/Product: plasminogen #status predicted <PRO>  
 F:1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>  
 F:1-77/Domain: activation peptide #status predicted <APT>  
 F:178-560/Product: plasmin chain A #status predicted <ACH>  
 F:84-162/Domain: kringle homology <KR1>  
 F:166-243/Domain: kringle homology <KR2>  
 F:256-333/Domain: kringle homology <KR3>  
 F:358-433/Domain: kringle homology <KR4>  
 F:450-790/Product: miniplasminogen #status experimental <MIN>  
 F:461-540/Domain: kringle homology <KR5>  
 F:561-790/Product: trypsin homology <TRY>  
 F:30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,307  
 bonds: #status predicted  
 F:602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 83.9%; Score 1292; DB 1; Length 790;  
 Best Local Similarity 81.4%; Pred. No. 2,4e-86;  
 Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

QY 1 VYLSECTGNGKNGKNGKNGITGCKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60

F:110-188/Domain: kringle homology <KR1>

A;Pathway: fibrinolysis  
C;Superfamily: plasmin; kringle homolo

A: description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the walls of the glomerular follicle; also activates the urokinase-type plasminogen activator  
 A: pathway: fibrinolysis  
 C: Superfamily: plasmin; kringlike homology; plasminogen-related protein precursor homology

C/Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd  
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-812/Product: plasminogen #status predicted <PRO>  
 F:20-96/Domain: activation peptide #status predicted <APT>  
 F:79-466/Product: angiotensin #status predicted <AST>  
 F:79-581,582-812/Product: plasmin #status predicted <WAT>  
 F:97-581/Domain: chain A #status predicted <ACH>  
 F:103-181/Domain: kringe homology <KR1>  
 F:185-262/Domain: kringe homology <KR2>  
 F:275-352/Domain: kringe homology <KR3>  
 F:377-454/Domain: kringe homology <KR4>  
 F:481-560/Domain: kringe homology <KR5>  
 F:582-812/Domain: chain B #status predicted <BCH>  
 F:582-805/Domain: trypsin homology <TRY>  
 F:59-73,55-61,103-161,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32  
 F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted  
 F:136-308/Binding site: carbonylate (Asn) (covalent) #status predicted  
 F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted  
 F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental  
 F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 82.7%; Score 1274; DB 1; Length 812;  
 Best Local Similarity 80.6%; Pred. No. 4,9e-85;  
 Matches 208; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

QY 1 VLSECKTGNKNGKNTGKSTKNGITCQKMSSTSPRRPSPATHPSEGLEENYCRNPND 60  
 DB 98 VLSECKTGNKNGKNTGKSTKNGITCQKMSSTSPRRPSPATHPSEGLEENYCRNPND 157  
 QY 61 DQGPWCYTTDPKRDYCDILECEBCHGSGENYDCKISKTMSGLCQAWDSOPPAH 120  
 DB 158 DEGPWCYTTDPKRDYCDILECEBCHGSGENYDCKISKTMSGLCQAWDSOPPAH 217  
 QY 121 GYPSFPPNKLKKNYCRNPDRRLPWCFTTDPKRMELCDIPRCTTPPSGPTQCL 180  
 DB 218 GYPSFPPNKLKKNYCRNPDRRLPWCFTTDPKRMELCDIPRCTTPPSGPTQCL 277  
 QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYCRNPDKRAFWCHT 240  
 DB 278 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYCRNPDKRAFWCHT 337  
 QY 241 TNSQVRMEYCKIPSCDS 258  
 DB 338 TDSQVRMEYCKIPSCDS 355

RESULT 6  
 146260  
 Plasmin (EC 3.4.21.7) precursor - western European hedgehog  
 C/Species: Echinacea europaea (western European hedgehog)  
 C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
 C/Accession: 146260  
 R/Law, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong  
 J. Biol. Chem. 270, 24004-24009, 1995  
 A/Title: The recurring evolution of lp(a): Insights from cloning of hedgehog apolipoprotein  
 A/Reference number: 146259; PMID:96025778; PMID:7592597  
 A/Accession: 146260  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-810 <LAW>  
 A/Cross-references: UNIPROT:Q29485; EMBL:U33171; NID:G1046360; PID:G1046361  
 C/Suprafamily: Plasmin; kringe homology; plasminogen-related protein precursor homology  
 C/Keywords: hydrolase; serine proteinase  
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>  
 F:103-181/Domain: kringe homology <KR1>  
 F:185-262/Domain: kringe homology <KR2>  
 F:275-352/Domain: kringe homology <KR3>  
 F:377-454/Domain: kringe homology <KR4>  
 F:481-561/Domain: kringe homology <KR5>  
 F:582-803/Domain: trypsin homology <TRY>

Query Match 80.3%; Score 1237; DB 2; Length 810;  
 Best Local Similarity 77.9%; Pred. No. 2.4e-82;  
 Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 VLSECKTGNKNGKNTGKSTKNGITCQKMSSTSPRRPSPATHPSEGLEENYCRNPND 60  
 DB 98 VLSECKTGNKNGKNTGKSTKNGITCQKMSSTSPRRPSPATHPSEGLEENYCRNPND 157  
 QY 61 DQGPWCYTTDPKRDYCDILECEBCHGSGENYDCKISKTMSGLCQAWDSOPPAH 120  
 DB 158 DEGPWCYTTDPKRDYCDILECEBCHGSGENYDCKISKTMSGLCQAWDSOPPAH 217  
 QY 121 GYPSFPPNKLKKNYCRNPDRRLPWCFTTDPKRMELCDIPRCTTPPSGPTQCL 180  
 DB 218 GYPSFPPNKLKKNYCRNPDRRLPWCFTTDPKRMELCDIPRCTTPPSGPTQCL 277  
 QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYCRNPDKRAFWCHT 240  
 DB 278 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYCRNPDKRAFWCHT 337  
 QY 241 TNSQVRMEYCKIPSCDS 258  
 DB 338 TNSQVRMEYCKIPSCDS 355

RESULT 7  
 118518  
 apolipoprotein(a) - western European hedgehog (fragment)  
 C/Species: Echinacea europaea (western European hedgehog)  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T18518  
 R/Law, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong  
 J. Biol. Chem. 270, 24004-24009, 1995  
 A/Title: The recurring evolution of lp(a): Insights from cloning of hedgehog apolipoprotein  
 A/Reference number: 146259; PMID:96025778; PMID:7592597  
 A/Accession: T18518  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-2869 <LAW>  
 A/Cross-references: UNIPROT:Q28398; EMBL:U33170; NID:G1046358; PID:G1046359; PIDN:AA648;  
 C/Experimental source: liver  
 C/Comment: The lipoprotein lp(a), a major inherited risk factor for atherosclerosis, coi  
 ent apolipoprotein(a).

Query Match 57.2%; Score 881; DB 2; Length 2869;  
 Best Local Similarity 55.0%; Pred. No. 5.6e-56;  
 Matches 149; Conservative 36; Mismatches 70; Indels 16; Gaps 3;

QY 3 LSECKTGNKNGKNTGKSTKNGITCQKMSSTSPRRPSPATHPSEGLEENYCRNPND 62  
 DB 2495 VDQCLEGEGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYCRNPDKRAFWCHT 2553  
 QY 63 DQGPWCYTTDPKRDYCDILECEBCHGSGENYDCKISKTMSGLCQAWDSOPPAH 110  
 DB 2554 VAPWCYTTNSAMREYCSIPACESPPTPEHLVVEBQCLBNGENYGNMAVITVSGPQCQ 2613  
 QY 111 AMDQSPHAGYISKPPNKLKKNYCRNPDRRLPWCFTTDPKRMELCDIPRCTTPPSGPTQCL 170  
 DB 2614 GMRKQTHRHRYTENTPNSKLPBNGYCRNPDRRLPWCFTTDPKRMELCDIPRCTTPPSGPTQCL 2673  
 QY 171 SSGPTV---OCLKGTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYCRNPDKRAFWCHT 227  
 DB 2674 PTEPMIIPDQCLEGEGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYCRNPDKRAFWCHT 2733  
 QY 228 RNPGRKAPNCHTNSQVRMEYCKIPSCDS 258  
 DB 2734 RNPGRKAPNCHTNSQVRMEYCKIPSCDS 2764

RESULT 8  
 280579  
 hepatocyte growth factor precursor [validated] - human  
 N/Alternate names: hepatopoietin A; scatter factor

C:Species: Homo sapiens (man)  
 C:Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #next change 09-Jul-2004  
 C:Accession: JH0579; J03033; A41140; B36677; A3512; A39006; PH0114; A37796; S06  
 R:Seki, T.; Hagiya, M.; Shimoniishi, M.; Nakamura, T.; Shimizu, S.  
 Gene 102, 213-219, 1991  
 A:Title: Organization of the human hepatocyte growth factor-encoding gene.  
 A:Reference number: JH0579; MUID:91340155; PMID:1831432  
 A:Accession: JH0579  
 A:Molecule type: DNA  
 A:Residues: 1-728 <SEK>  
 A:Cross-references: UNIPROT:P14210, DDBJ:D90318  
 A>Note: the authors translated the codon GAA for residue 662 as Gly  
 R:Seki, T.; Hagiya, M.; Shimoniishi, M.; Nakamura, T.; Shimizu, S.  
 submitted to JIJD, March 1991  
 A:Description: Organization of the human hepatocyte growth factor-encoding gene.  
 A:Reference number: J03033  
 A:Accession: J03033  
 A:Molecule type: DNA  
 A:Residues: 1-481, 'RT', 484-728 <SE2>  
 R:Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991  
 A:Title: Evidence for the identity of human scatter factor and human hepatocyte growth factor.  
 A:Reference number: A41140; MUID:91334393; PMID:1831266  
 A:Accession: A41140  
 A:Molecule type: mRNA  
 A:Residues: 1-728 <ME1>  
 A:Cross-references: GB:M73239; NID:G337935; PIDN:AAA64239.1; PID:G337935  
 R:Seki, T.; Ihara, I.; Sugimura, A.; Shimoniishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M.  
 Biochem. Biophys. Res. Commun. 172, 321-327, 1990  
 A:Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor.  
 A:Reference number: A36677; MUID:91025062; PMID:2145836  
 A:Accession: B36677  
 A:Molecule type: mRNA  
 A:Residues: 1-728 <SE3>  
 A:Cross-references: GB:M60718; NID:G184031; PIDN:AAA52648.1; PID:G184032  
 A:Accession: A36677  
 A:Molecule type: mRNA  
 A:Residues: 1-161, 167-728 <SE4>  
 A:Cross-references: EMBL:X16323  
 A:Experimental source: leukocyte  
 R:Myazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya  
 Biochem. Biophys. Res. Commun. 163, 967-973, 1989  
 A:Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth factor.  
 A:Reference number: A3512; MUID:89392017; PMID:2528952  
 A:Accession: A3512  
 A:Molecule type: mRNA  
 A:Status: not compared with conceptual translation  
 A:Note: does not have proteinase activity  
 C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringlike homol  
 C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringlike; py  
 F:1-31/Domain: signal sequence #status predicted <SIG>  
 F:32-494/Domain: alpha chain #status predicted <MAT>  
 F:128-206/Domain: kringlike homology <KR1>  
 F:211-288/Domain: kringlike homology <KR2>  
 F:305-383/Domain: kringlike homology <KR3>  
 F:391-469/Domain: kringlike homology <KR4>  
 F:455-728/Domain: beta chain #status experimental <BCH>  
 F:455-716/Domain: tryptidomoloy carbonylic acid (Gln) (in mature form) #status experime  
 F:294/402, 566, 653/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:487-604/Disulfide bonds: #status predicted

R:Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimoniishi, M.; Sugimura, A.; Tash  
 Nature 342, 440-443, 1989  
 A:Title: Molecular cloning and expression of human hepatocyte growth factor.  
 A:Reference number: S06794; MUID:90066676; PMID:2531289  
 A:Accession: S06794  
 A:Molecule type: mRNA  
 A:Residues: 1-31, 'HK', 34-77, 'N', 79-292, 'V', 294-299, 'W', 301-316, 'A', 318-335, 'K', 337-386,  
 A:Cross-references: EMBL:X16323; NID:G32081; PIDN:CAA34387.1; PID:G32082  
 A:Experimental source: liver  
 A:Note: the authors translated the codon CAG for residue 727 as Glu  
 R:Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birch  
 Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992  
 A:Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fac  
 A:Reference number: I59214; MUID:93087571; PMID:1280830  
 A:Accession: I59214  
 A:Molecule type: mRNA  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 1-288, 'ET' <HAR>  
 A:Cross-references: GB:I02931; NID:G184033; PIDN:AAA52649.1; PID:G184034  
 R:Myazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.  
 Eur. J. Biochem. 197, 15-22, 1991  
 A:Title: An alternatively processed mRNA generated from human hepatocyte growth factor  
 A:Reference number: S15443; MUID:91200041; PMID:1826653  
 A:Accession: S15443  
 A:Molecule type: mRNA  
 A:Status: preliminary  
 A:Residues: 1-288, 'ET' <MY2>  
 A:Cross-references: EMBL:X57574; NID:G32083; PIDN:CAA40802.1; PID:G32084  
 R:Shima, N.; Nagao, M.; Ogaki, F.; Teuda, E.; Murakami, A.; Higashio, K.  
 Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991  
 A:Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning  
 A:Reference number: I52253; MUID:92062058; PMID:1835383  
 A:Accession: I52253  
 A:Molecule type: mRNA  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 161-166 <SHI>  
 A:Cross-references: GB:S62561; NID:G237996; PIDN:AA820169.1; PID:G237997  
 C:Genetics:  
 A:Gene: GDB:HGFP  
 A:Cross-references: GDB:127524; OMIM:142409  
 A:Map position: 7q21.1-7q21.1  
 A:Insertions: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 4  
 C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
 C:Function:  
 A:Description: stimulates mitosis of hepatocytes and other cells  
 A:Note: does not have proteinase activity  
 C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringlike homol  
 C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringlike; py  
 F:1-31/Domain: signal sequence #status predicted <SIG>  
 F:32-494/Domain: alpha chain #status predicted <MAT>  
 F:128-206/Domain: kringlike homology <KR1>  
 F:211-288/Domain: kringlike homology <KR2>  
 F:305-383/Domain: kringlike homology <KR3>  
 F:391-469/Domain: kringlike homology <KR4>  
 F:455-728/Domain: beta chain #status experimental <BCH>  
 F:455-716/Domain: tryptidomoloy carbonylic acid (Gln) (in mature form) #status experime  
 F:294/402, 566, 653/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:487-604/Disulfide bonds: #status predicted

Query Match 51.8%; Score 797; DB 1; Length 728;  
 Best Local Similarity 51.0%; Pred. No. 1,8e-50;  
 Matches 134; Conservative 42; Mismatches 81; Indels 6; Gaps 4;

Oy 2 YLSECTGNGKXVYRGTSTKNGITGCKXSSSTSPRRSPATHPSEGLBENYCRPND 61  
 Db 124 YINACILGKGRSKXGVSTKSGIKQCPSSMTPHNSHSLPSSYRKQIDENYCRPRGE 183  
 Oy 62 POGPCVYTDPEKRYDYCDLSECE-ECMKGSGENTGKISKTMGLGECQAMDSQSPAH 120  
 Db 184 EGSPWCFSTSNPEVRYEVCIDPQCEVEVCMTGNGESYRGLMDHTESGKICQRMHDQPRHR 243



QY 121 GYIPSPKPNKLNKKYCNCRNPDRLELPKCFITTPDKRRELCDIPRC--TTPPSSGP--TY 176  
DB 244 KFLPERYPDKGFDDNCCNPDGKRPKCYTLDPDTPMEYCAIKMCAHSAVNETDPMF-- 302  
QY 177 OCLKGTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLIDENYCRNPDGR 234  
DB 304 ECTGGGEGYRGVNTIWMGIPCORWDSQYPHHDITPENFKCKDLRENYCRNPDGSESP 362  
QY 237 WCHTNSQVMEYC-KIPSCDS 258  
DB 364 WCFTTDPNIRVGYCSQIPKCDVS 387

## RESULT 9

A35644  
hepatocyte growth factor precursor - rat  
N/Alternate names: hepatoin A; scatter factor  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 28-Sep-1990 #sequence\_revision 18-Nov-1992 #text\_change 09-Jul-2004  
C/Accession: A35644; S13211  
R/Taishiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimomishi, M.; Shimizu, S.; Nakamura  
Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990  
A/Title: Deduced primary structure of rat hepatocyte growth factor and expression of the  
A/Reference number: A35644; MUID:90222197; PMID:2139229  
A/Accession: A35644  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-728 <TAS>  
A/Cross-references: UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA14133.1;  
R/Okaizumi, A.; Miyazawa, K.; Kitamura, N.  
Eur. J. Biochem. 193, 375-381, 1990  
A/Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA dur  
A/Reference number: S13211; MUID:91031482; PMID:2146117  
A/Accession: S13211  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-728 <OKA>  
A/Cross-references: EMBL:X54400; NID:956353; PIDN:CAA38266.1; PID:94539554  
C/Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C/Function:  
A/Description: stimulates mitosis of hepatocytes and other cells  
A/Note: does not have proteinase activity  
C/Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo  
C/Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr  
F.1-32/Domain: signal sequence #status predicted <SIG>  
F.56-495/Product: hepatocyte growth factor #status predicted <MAT>  
F.129-207/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>  
F.212-289/Domain: kringle homology <KR1>  
F.306-384/Domain: kringle homology <KR2>  
F.392-470/Domain: kringle homology <KR3>  
F.496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>  
F.53/Modified site: pyroglutamate carboxylate (Asn) (in mature form) #status predicted  
F.595,566/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F.488-607/Disulfide bonds: #status predicted

Query Match 50.8%; Score 782; DB 1; Length 728;  
Best Local Similarity 49.8%; Pred. No. 2,2e-49;  
Matches 132; Conservative 39; Mismatches 84; Indels 10; Gaps 4;

QY 2 YLSECKTGNGKNGYGTMSKTNGITCOKMSSTSPHPRPSPATHPEGLSENYCRNPND 61  
DB 125 YIRNCTIGKGSNGYGTMSKTNGITCOKMSSTSPHPRPSPATHPEGLSENYCRNPND 184  
QY 62 POGPMCTTDPKRYDYCDILECEE-ECMHGSGENYDGKISKTMSGLECOAQWDSQSPAH 120  
DB 185 EGGPMCFSTNPEVRYEVCIDPQCSVEVCMTGNGSYRGPMHDSGKTQWRDQGRPHH 244  
QY 121 GYIPSPKPNKLNKKYCNCRNPDRLELPKCFITTPDKRRELCDIPRC--TTPPSSGP 174

DB 245 KFLPERYPDKGFDDNCCNPDGKRPKCYTLDPDTPMEYCAIKMCAHSAVNETDPMF-- 302  
QY 175 TYOCLKGTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLIDENYCRNPDGR 234  
DB 303 TTECIKGGEGYRGVNTIWMGIPCORWDSQYPHHDITPENFKCKDLRENYCRNPDGAE 362  
QY 235 APWCHTNSQVMEYC-KIPSCDS 258  
DB 363 SPWCFTTDPNIRVGYCSQIPKCDVS 387

## RESULT 10

151283  
hepatocyte growth factor precursor - clawed frog  
N/Alternate names: hepatoin A; scatter factor  
C/Species: Xenopus sp. (clawed frog)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-May-2004  
C/Accession: 151283  
R/Nakamura, H.; Taishiro, K.; Nakamura, T.; Shiohara, K.  
Mol. Cell. Dev. 49, 123-131, 1995  
A/Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus ea  
A/Reference number: 151283; MUID:95267690; PMID:7748783  
A/Accession: 151283  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-710 <NAR>  
A/Cross-references: GB:S77422; NID:9998932; PIDN:AB34354.1; PID:9998933  
A/Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucleot  
C/Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C/Function:  
A/Description: stimulates mitosis of hepatocytes and other cells  
A/Note: does not have proteinase activity  
C/Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo  
C/Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle  
F.42-477, 478-709/Product: hepatocyte growth factor #status predicted <MAT>  
F.115-193/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>  
F.198-275/Domain: kringle homology <KR1>  
F.289-367/Domain: kringle homology <KR2>  
F.375-453/Domain: kringle homology <KR3>  
F.478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCH>  
F.52,128,281,322,379,550,637,666/Binding site: carbohydrate (Asn) (covalent) #status pr  
F.470-588/Disulfide bonds: #status predicted

Query Match 50.4%; Score 776.5; DB 1; Length 710;  
Best Local Similarity 50.0%; Pred. No. 5.4e-49;  
Matches 130; Conservative 39; Mismatches 88; Indels 3; Gaps 3;

QY 2 YLSECKTGNGKNGYGTMSKTNGITCOKMSSTSPHPRPSPATHPEGLSENYCRNPND 61  
DB 111 YIRNCTIGKGSNGYGTMSKTNGITCOKMSSTSPHPRPSPATHPEGLSENYCRNPND 170  
QY 62 POGPMCTTDPKRYDYCDILECEE-ECMHGSGENYDGKISKTMSGLECOAQWDSQSPAH 120  
DB 171 EGGPMCFSTNPEVRYEVCIDPQCSVEVCMTGNGSYRGPMHDSGKTQWRDQGRPHH 230  
QY 121 GYIPSPKPNKLNKKYCNCRNPDRLELPKCFITTPDKRRELCDIPRC--TTPPSSGP 179  
DB 231 KFLPERYPDKGFDDNCCNPDGKRPKCYTLDPDTPMEYCAIKMCAHSAVNETDPMF-- 290  
QY 180 KGTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLIDENYCRNPDGRAPCH 239  
DB 291 KGGEGYRGVNTIWMGIPCORWDSQYPHHDITPENFKCKDLRENYCRNPDGSESPCF 350  
QY 240 TTSQVMEYC-KIPSCDS 258  
DB 351 TTDNIRIGHGCSQIKKCOAS 370

## RESULT 11

A60185  
hepatocyte growth factor precursor - mouse



N:Alternate names: hepatocetin A:scatter factor  
C:Species: Mus musculus (house mouse)  
C>Date: 03-Mar-1993 #sequence revision 26-May-1994 #ext change 09-Jul-2004  
C:Accession: J02117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758; J00231  
R:Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.  
Biochem. Biophys. Res. Commun. 199, 772-779, 1994  
A>Title: Identification of mouse mammary fibroblast-derived mammary growth factor as hep  
A:Reference number: J02117; MUID:94183257; PMID:8135822  
A:Accession: J02117  
A:Molecule type: mRNA  
A:Residues: 1-728 <SAS2>  
A:Cross-references: UNIPROT:008048; GB:D10212; NID:9220435; PIDN:BA01064.1; PID:9220436  
A:Experimental source: fibroblast, COS-1 cell  
A>Note: submitted to JIPID, May 1993  
A:Accession: PC2064  
A:Molecule type: protein  
A:Residues: 496-504 <SAS2>  
R:Rosen, E.M.; Meromsky, L.; Selter, E.; Vinter, D.W.; Goldberg, I.D.  
Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990  
A>Title: Purified scatter factor stimulates epithelial and vascular endothelial cell mig  
A:Reference number: A60185; MUID:90377927; PMID:2144630  
A:Accession: A60185  
A:Molecule type: protein  
A:Residues: 'X',184-188,'KX',191-192,'X',194,'XX',197,357-364,'XX',367,375-377,'E',379,'  
R:Lin, Y., Michalopoulos, G.K.; Zarnegar, R.  
Biochim. Biophys. Acta 1216, 299-303, 1993  
A>Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth  
A:Reference number: S43416; MUID:94060105; PMID:8241272  
A:Accession: S43416  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-728 <LID>  
A:Cross-references: EMBL:X72307  
R:Lin, Y.  
submitted to the EMBL Data Library, May 1993  
A:Reference number: S45521  
A:Accession: S45521  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-563,'H',565-728 <LID>  
A:Cross-references: EMBL:X72307  
R:Coffey, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.  
Biochem. J. 278, 35-41, 1991  
A>Title: Purification and characterization of biologically active scatter factor from ra  
A:Reference number: S17173; MUID:91354223; PMID:1831975  
A:Accession: S17173  
A:Molecule type: protein  
A:Residues: 496-517,'T',519 <COR>  
R:Gherardi, E.; Stoker, M.  
Nature 346, 228, 1990  
A>Title: Hepatocytes and scatter factor.  
A:Reference number: S10966; MUID:90326152; PMID:2142751  
A:Accession: S10966  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 456-507,'X',509-512,'L',514-516,'X',518-519 <NAT>  
R:Plaschke-Schluter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.  
J. Biol. Chem. 270, 830-836, 1995  
A>Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.  
A:Reference number: I48758; MUID:95125332; PMID:7822318  
A:Accession: I48758  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-30 <RBS>  
A:Cross-references: EMBL:X81630; NID:9673451; PIDN:CA557266.1; PID:9673452  
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C:Function:  
A:Description: stimulates mitosis of hepatocytes and other cells  
A>Note: does not have proteinase activity  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homol  
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; PYT  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:56-495,496-728/Product: hepatocyte growth factor #status predicted <MAT>

F:56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>  
F:129-207/Domain: kringle homology <KR1>  
F:212-289/Domain: kringle homology <KR2>  
F:306-384/Domain: kringle homology <KR3>  
F:392-470/Domain: kringle homology <KR4>  
F:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>  
F:496-719/Domain: trypsin homology <TRY>  
F:33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predi  
F:295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:488-607/Disulfide bonds: #status predicted

Query Match 50.4%; Score 776; DB 1; Length 728;  
Best Local Similarity 49.4%; Pred. No. 66-49;  
Matches 131; Conservative 40; Mismatches 84; Indels 10; Gaps 4;

QY 2 YLSECKTGKNGKRYGKMTSKNGITCOAKSSSTSPHPPSPATHPSEGLBENYCRPNDD 61  
D 125 YINCCIIGKGGSYKGVSTIKSGIKQPNVSMFPHHSFLPSSYRGRKDQENYCRPNRGE 184  
QY 62 PGSPWCYTTDPKRYDYCDILECEE-ECMHSGENYDGKISKTMGLCOAMDSPHAF 120  
D 185 EGSPWCFTSNPEVRYEVCIDPQCSVEVCMTNGESTYRGPMDHTESKTCORWDQTPHRH 244  
QY 121 GYIPKSPNNKLNKYNCRNPDELRLPWCFTTDPNKRWELCDIPRCT-----TPPSSGP 174  
D 245 KFLPERYPDKGPDNDYCRNPDGKRPWCYTLDPDTFWEICAITCAHSVNETDVME-- 302  
QY 175 TYOCLKGKGTGNNYGVAVYVSGTCQWMSAQTPHTERPPENPCNLDENYCRNPDGKR 234  
D 303 TTECIQGGEGYGTGNTIWNIGIPCORWDSQYPHKHIDITPENKCKDLRENNYCRNPDGAE 362  
QY 235 APWCHTTNSQVRWYEC-KIPSCDSS 258  
D 363 SPWCFTTDPNIRKYGCSQIPKCDVS 387

## RESULT 12

J05061  
macrophage-stimulating protein 1 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #ext change 09-Jul-2004  
C:Accession: J05061  
R:Ohshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takaue,  
Biochem. Biophys. Res. Commun. 227, 273-280, 1996  
A>Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in  
A:Reference number: J05061; MUID:97011126; PMID:8858136  
A:Accession: J05061  
A:Molecule type: mRNA  
A:Residues: 1-716 <OHS>  
A:Cross-references: UNIPROT:P70521; EMBL:X95096; NID:91669718; PIDN:CA64473.1; PID:916  
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homol  
C:Keywords: duplication; glycoprotein; growth factor; kringle  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <MAT>  
F:32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>  
F:110-186/Domain: kringle homology <KR1>  
F:191-268/Domain: kringle homology <KR2>  
F:292-370/Domain: kringle homology <KR3>  
F:379-457/Domain: kringle homology <KR4>  
F:489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>  
F:489-709/Domain: trypsin homology <TRY>  
F:72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.8%; Score 766.5; DB 1; Length 716;  
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Matches 132; Conservative 36; Mismatches 89; Indels 15; Gaps 5;

QY 2 YLSECKTGKNGKRYGKMTSKNGITCOAKSSSTSPHPPSPATHPSEGLBENYCRPNDD 61  
D 106 YVTCIMDGAASYRGTAVATADGLPCQAWSRFPNDHKTPT--PKNGLEENPCRNPD 163  
QY 62 PGSPWCYTTDPKRYDYCDILECEE-ECMHSGENYDGKISKTMGLCOAMDSPHAF 120

RESULT 14  
 A40332  
 macrophage-stimulating protein 1 precursor - mouse  
 N.Alternate names: hepatocyte growth factor-like protein  
 C.Species: Mus musculus (house mouse)  
 C.Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
 C.Accession: A40332; B40332  
 R.Degen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.  
 Biochemistry 30, 9781-9791, 1991  
 A.Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor  
 A.Reference number: A40332; MUID:92002017; PMID:1832957  
 A.Accession: A40332

A:Residues:1-4548 <MC>  
A:Cross-references: UNIPROT:P08519, GB:X06290, EMBL:X06596, NID:g28619, PIDD:CAA29618.1,  
R:Batton, D.L.; Fless, G.W.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.,  
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987  
A:Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to  
A:Reference number: A28017, MUID:87204109, PMID:3472206  
A:Accession: A28017  
A:Molecule type: protein  
A:Residues: 20-21, 'E', 23-34, 177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200-292-314, 'W', 316-31  
X, '4396-4401 <EAT>  
R:Mede, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zybrow, B.R.; Meer, K.; Schwartz, K  
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993

```

F:2292-3069/Domain: kringle homology <KR27>
F:3106-3183/Domain: kringle homology <KR28>
F:3220-3297/Domain: kringle homology <KR29>
F:3334-3411/Domain: kringle homology <KR30>
F:3448-3525/Domain: kringle homology <KR31>
F:3562-3639/Domain: kringle homology <KR32>
F:3676-3753/Domain: kringle homology <KR33>
F:3782-3859/Domain: kringle homology <KR34>
F:3896-3973/Domain: kringle homology <KR35>
F:4010-4087/Domain: kringle homology <KR36>
F:4124-4201/Domain: kringle homology <KR37>
F:4228-4307/Domain: kringle homology <KR38>
F:4328-4541/Domain: trypsin homology <TRY>

Query Match          48.6%; Score 749; DB 1; Length 4548;
Best Local Similarity 41.2%; Pred. No. 3.3e-46;
Matches 129; Conservative 45; Mismatches 81; Indels 58; Gaps 5;

QY      3  LSEKTKNGKNGYKGTMSKTKNGILTCQKWSSTSPHRRPFPSPATHPSEGLEENYCRNPNDP 62
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      3779  VODCYHGDGQSYRGSFSTIYTGRTQCSWSSMTPHMHQRTTEYYPNGLITRNYCRNPDAEI 3838

QY      63  QGPMCYTTDEKRYDYDCDILECE-----BECM 89
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      3839  R-PWCTYMDPSVWMEYCNLTQCPEVMESTLLTPTVVPVSTELPSEAPTEENSTGVDDCY 3897

QY      90  HCSGENYDGIKISKTMGSLGECQAMDSQSPHAGYIPSKFPNKNLKONYCRNPDRRLRPWCF 149
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      3898  RGGQGSYRGTLSTTIITRTQCSWSSMTPHMHKRIPLYPNAGLITRNYCRNPDAEIRFWCY 3957

QY      150  TTDPNKRWELCDIIPRC-----TTP-----PSSGPTYQ-CLKGTGEN 185
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      3958  TMDPSVWMEYCNLTQCPVTESSVILTPTVAPVPSTEARSEQAPPEKSPVQDDCYHGDGRS 4017

QY      186  YRGNAVAVTVSGHTCOHMSAQTPHTHETEPNPFCKNLDENYCRNPDGKRAPWCHITTSQV 245
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      4018  YRGISSTTVYGRTCQSSMSIPIPHQRTPEPNYPNAGLITENYCRNPDSGKQPMCYTTDPCV 4077

QY      246  RMEYCKIPSCDS 258
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      4078  RMEYCNLTQCSER 4090

Search completed: July 27, 2005, 03:30:30
Job time : 17 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 03:21:14 ; Search time 61 Seconds

(without alignments)  
2182.633 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGNGKRYRGTMK.....TNSQVAREYCKIPSCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1535	99.7	810	1	PLMN_HUMAN
2	1442	93.6	810	1	PLMN_MACMU
3	1306	84.8	359	2	08WMRI
4	1293	84.4	812	1	PLMN_RAT
5	1292	83.9	790	1	PLMN_PIG
6	1291	83.8	812	1	PLMN_BOVIN
7	1279	83.1	466	2	06TCIO
8	1279	83.1	812	1	PLMN_MOUSE
9	1237	80.3	810	1	PLMN_ERIEU
10	1203.5	78.1	759	2	07TP84
11	1160	75.3	806	1	PLMN_MACCU
12	996	64.7	818	2	06PBA6
13	881	57.2	2869	2	028398
14	809.5	52.6	449	2	06GPI4
15	809.5	52.6	716	2	091691
16	797	51.8	728	1	HGF_HUMAN
17	796	51.7	709	2	07ZTN9
18	795.5	51.7	717	2	P70006
19	782	50.8	728	1	HGF_RAT
20	778	50.5	726	2	090578
21	778	50.5	730	2	086787
22	777	50.5	728	2	086787
23	776.5	50.4	710	2	086787
24	776	50.4	728	1	HGF_MOUSE
25	774	50.3	730	2	076851
26	772	50.1	704	2	090865
27	772	50.1	728	2	090865
28	766.5	49.8	709	2	0902N6
29	766.5	49.8	716	2	P70521
30	754.5	49.0	405	2	0788Q2
31	753.5	48.9	716	1	HGFL_MOUSE

#### ALIGNMENTS

32	753.5	48.9	716	2	091XG8	091XG8 mus musculus
33	749	48.6	4548	1	AP0A_HUMAN	P08519 homo sapien
34	739	48.0	711	1	HGFL_HUMAN	P26927 homo sapien
35	739	48.0	1420	1	AP0A_MACMU	P14417 macaca mula
36	709	46.0	567	2	013208	013208 homo sapien
37	643	41.8	648	2	09H1V4	09H1V4 homo sapien
38	503	32.7	454	2	046506	046506 papio hamad
39	459.5	29.8	215	2	042341	042341 gallus gall
40	458.5	29.8	429	2	08AVB0	08AVB0 brachydanto
41	412.5	26.8	615	2	06GNK4	06GNK4 xenopus lae
42	407.5	26.5	607	2	06DFJ5	06DFJ5 xenopus lae
43	400	26.0	209	2	08BS17	08BS17 mus musculus
44	391.5	25.4	325	2	PLMN_PETMA	P33574 petromyzon
45	383	24.9	948	2	0911Y6	0911Y6 ephydactia f

#### RESULT 1

ID	PLMN_HUMAN	STANDARD;	PRT;	810 AA.
AC	P00747; O15146; O6PA00;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].			
GN	Name=PLG;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND VARIANT ASN-472.			
RX	MEDLINE=90202879; PubMed=2318848;			
RA	Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;			
RT	"Characterization of the gene for human plasminogen, a key proenzyme			
RT	in the fibrinolytic system.";			
RT	J. Biol. Chem. 265:6104-6111(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87162490; PubMed=3030813; DOI=10.1016/0014-5793(87)81501-6;			
RA	Forrester M., Raden B., Israelsson M., Larsson K., Heden L.-O.;			
RT	"Molecular cloning and characterization of a full-length cDNA clone			
RT	for human plasminogen.";			
RT	FEBS Lett. 213:254-260(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,			
RA	Mitchell D., Robinson J.H.;			
RT	"Expression of recombinant human plasminogen and aglycoplasminogen in			
RT	HeLa cells.";			
RT	Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANTS LYS-57; GLN-133; HIS-261; TRP-408;			
RP	ASN-472; VAL-494 AND TRP-523.			
RA	Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,			
RA	Rajkumar N., Torch E.J., Yi Q., Nickerson D.A.;			
RT	"Sequences, NIDB HL66682 program for genomic applications, UW-			
RT	PHRC, Seattle, WA (URL: http://pga.gs.washington.edu)." ;			
RT	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=23386257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Dicicchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,			
RA	Brownstein M.J., Uedlin T.B., Toehiyuki S., Carninci P., Prange C.,			

- RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smalhus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP SEQUENCE OF 20-810, AND VARIANT ASN-472.  
 RA Sottrup-Jensen L., Petersen T.E., Magnusson S.;  
 RL Submitted (JUL-1977) to the PIR data bank.  
 RN [7]  
 RP SEQUENCE OF 292-810 FROM N.A.  
 RA MEDLINE=85023311; PubMed=6148961;  
 RA Malinowski D.P., Sadler J.E., Davie E.W.;  
 RT "Characterization of a complementary deoxyribonucleic acid coding for  
 RT human and bovine plasminogen.";  
 RL Biochemistry 23:4243-4250(1984).  
 RN [8]  
 RP SEQUENCE OF 20-100.  
 RA MEDLINE=75093329; PubMed=122932;  
 RA Wiman B., Wallen P.;  
 RT "Structural relationship between 'glutamic acid' and 'lysine' forms of  
 RT human plasminogen and their interaction with the NH2-terminal  
 RT activation peptide as studied by affinity chromatography.";  
 RL Eur. J. Biochem. 50:489-494(1975).  
 RN [9]  
 RP SEQUENCE OF 95-380; 581-626; 657-700 AND 732-810, AND VARIANT ASN-472.  
 RA Sottrup-Jensen L., Claess H., Zaidel M., Petersen T.E., Magnusson S.;  
 RA (in) Davidson J.F., Kovacs R.M., Samama M.M., Desnoyers P.C. (eds.);  
 RT Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,  
 RL Raven Press, New York (1978).  
 RN [10]  
 RP SEQUENCE OF 483-604.  
 RA MEDLINE=76043692; PubMed=126863;  
 RA Wiman B., Wallen P.;  
 RT "Amino-acid sequence of the cyanogen-bromide fragment from human  
 RT plasminogen that forms the linkage between the plasmin chains.";  
 RL Eur. J. Biochem. 58:539-547(1975).  
 RN [11]  
 RP SEQUENCE OF 581-810.  
 RA MEDLINE=77225245; PubMed=142009;  
 RA Wiman B.;  
 RT "Primary structure of the B-chain of human plasmin.";  
 RL Eur. J. Biochem. 76:129-137(1977).  
 RN [12]  
 RP ACTIVE SITE.  
 RA MEDLINE=73149248; PubMed=4694729;  
 RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;  
 RT "The primary structure of human plasminogen. II. The histidine loop of  
 RT human plasmin: 119nt (B) chain active center histidine sequence.";  
 RL J. Biol. Chem. 248:1631-1633(1973).  
 RN [13]  
 RP ACTIVE SITE.  
 RA MEDLINE=69234739; PubMed=4240117;  
 RA Groskopf W.R., Summaria L., Robbins K.C.;  
 RT "Studies on the active center of human plasmin. Partial amino acid  
 RT sequence of a peptide containing the active center serine residue.";  
 RL J. Biol. Chem. 244:3590-3597(1969).  
 RN [14]  
 RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.  
 RA MEDLINE=82213905; PubMed=6919539;  
 RA Trexler M., Vail Z., Patchy L.;  
 RT "Structure of the omega-aminocarboxylic acid-binding sites of human  
 RT plasminogen. Arginine 70 and aspartic acid 56 are essential for  
 RT binding of ligand by kringle 4.";  
 RL J. Biol. Chem. 257:7401-7406(1982).
- RN [15]  
 RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.  
 RX MEDLINE=85054794; PubMed=6094526;  
 RA Vail Z., Patchy L.;  
 RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34 are  
 RT essential for fibrin affinity of the kringle 1 domain.";  
 RL J. Biol. Chem. 259:13690-13694(1984).  
 RN [16]  
 RP PHOSPHORYLATION SITE SER-597.  
 RX MEDLINE=97345939; PubMed=9201958; DOI=10.1021/bi970328d;  
 RA Wang H., Piorok M., Bretthauer R.K., Castellino F.J.;  
 RT "Serine-578 is a major phosphorylation locus in human plasma  
 RT plasminogen.";  
 RL Biochemistry 36:8100-8106(1997).  
 RN [17]  
 RP CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=88185329; PubMed=3356193;  
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,  
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;  
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine  
 RT plasminogen. Species specificity in relation to stialylation and  
 RT fucosylation patterns.";  
 RL Eur. J. Biochem. 173:57-63(1988).  
 RN [18]  
 RP CARBOHYDRATE-LINKAGE SITE SER-268.  
 RX MEDLINE=97207306; PubMed=9054441; DOI=10.1074/jbc.272.11.7408;  
 RA Pirte-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,  
 RA Pizzo S.V.;  
 RT "Evidence for a novel O-linked stialylated trisaccharide on Ser-248 of  
 RT human plasminogen 2.";  
 RL J. Biol. Chem. 272:7408-7411(1997).  
 RN [19]  
 RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.  
 RX MEDLINE=95042728; PubMed=7525077; DOI=10.1016/0092-8674(94)90200-3;  
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,  
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;  
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the  
 RT suppression of metastases by a Lewis lung carcinoma.";  
 RL Cell 79:315-328(1994).  
 RN [20]  
 RP CHARACTERIZATION OF ANGIOSTATIN.  
 RX MEDLINE=97238710; PubMed=9102221;  
 RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Maden J.W.,  
 RA Lapcevich R., Nacy C.A.;  
 RT "A recombinant human angiostatin protein inhibits experimental primary  
 RT and metastatic cancer.";  
 RL Cancer Res. 57:1329-1334(1997).  
 RN [21]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.  
 RX MEDLINE=92031502; PubMed=1657148;  
 RA Muliach A.M., Tulinaky A., Ravichandran K.G.;  
 RT "Crystal and molecular structure of human plasminogen kringle 4  
 RT refined at 1.9-A resolution.";  
 RL Biochemistry 30:10576-10586(1991).  
 RN [22]  
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.  
 RX MEDLINE=92031503; PubMed=1657149;  
 RA Wu T.-P., Padmanabhan K., Tulinaky A., Muliach A.M.;  
 RT "The refined structure of the epsilon-aminocaproic acid complex of  
 RT human plasminogen kringle 4.";  
 RL Biochemistry 30:10589-10594(1991).  
 RN [23]  
 RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.  
 RX MEDLINE=15299951;  
 RA Stec B., Yamano A., Whitlow M., Teeter M.M.;  
 RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.  
 RT A possible structural role of disordered residues.";  
 RL Acta Crystallogr. D 53:169-178(1997).  
 RN [24]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.  
 RX MEDLINE=96180681; PubMed=8611560; DOI=10.1021/bi952135i;  
 RA Mathews I.I., Vanderhoff-Hanover P., Castellino F.J., Tulinaky A.;  
 RT "Crystal structures of the recombinant kringle 1 domain of human



FT DISULFID 296 335 By similarity.  
 FT DISULFID 324 347 By similarity.  
 FT DISULFID 377 454 By similarity.  
 FT DISULFID 398 437 By similarity.  
 FT DISULFID 426 449 By similarity.  
 FT DISULFID 481 560 By similarity.  
 FT DISULFID 502 543 By similarity.  
 FT DISULFID 531 555 By similarity.  
 FT DISULFID 567 685 Interchain (By similarity).  
 FT DISULFID 577 585 Interchain (By similarity).  
 FT DISULFID 607 623 By similarity.  
 FT DISULFID 699 766 By similarity.  
 FT DISULFID 729 745 By similarity.  
 FT DISULFID 756 784 By similarity.  
 FT CARBOHYD 365 365 O-linked (GlcNAc...) (By similarity).  
 SQ SEQUENCE 810 AA; 90255 MW; A75E1C51A1A0F24A CRC64;

Query Match 93.6%; Score 1442; DB 1; Length 810;  
 Best Local Similarity 93.1%; Pred. No. 1.3e-101;  
 Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 VYLSECKTGKNGKRYGTMSKTKNGITCOKWSSTSPHRRPSPATHPSEGLSENYCRNPDN 60  
 |||  
 DB 98 VYLSECKTGKNGKRYGTMSKTKNGITCOKWSSTSPHRRPSPATHPSEGLSENYCRNPDN 157  
 |||

QY 61 DPGPMCYTTDPPEKRYDYCDILECEEECHMGSGENYDGIKSKTMSGLECOAMDSPHAA 120  
 |||  
 DB 158 DPGPMCYTTDPPEKRYDYCDILECEEECHMGSGENYDGIKSKTMSGLECOAMDSPHAA 217  
 |||

QY 121 GYIPSKFPKNIKKNKCRNPDELRPWCFTTDPNKRWEICDIPRCTTPPPSGPTTQCCLK 180  
 |||  
 DB 218 GYIPSKFPKNIKKNKCRNPDELRPWCFTTDPNKRWEICDIPRCTTPPPSGPTTQCCLK 277  
 |||

QY 181 GTGENYRGNAVAVYSGHTCOHWSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCYT 240  
 |||  
 DB 278 GTGENYRGNAVAVYSGHTCOHWSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCYT 337  
 |||

QY 241 TNSQVRWEYCKIPSCDSSPV 260  
 |||  
 DB 338 TNSQVRWEYCKIPSCDSSPV 357  
 |||

RESULT 3  
 Q8WMR1 PRELIMINARY; PRT; 359 AA.  
 AC Q8WMR1;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Plasmalogen (Fragment).  
 DE Canis familiaris (Dog).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NX NCBI\_Taxid=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pitte-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O.,  
 RA Folkman J., Waters D.J.;  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY069985; AAL58519.1; -;  
 DR HSPF, P00747; IPMK.  
 DR GO: GO:0005509; F:calcium ion binding; IEA.  
 DR GO: GO:0003809; F:thrombin activity; IEA.  
 DR GO: GO:0007596; P:blood coagulation; IEA.  
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR Pfam: PF00051; Kringle\_4.  
 DR PRINTS: PRO0018; Kringle\_4.  
 DR PRINTS: PRO1505; PROTHROMBIN.  
 DR PRODOM: PD000395; Kringle\_4.  
 DR SMART: SM00130; KR; 4.  
 DR PROSITE: PS00021; KRINGLE\_1; 4.  
 DR PROSITE: PS00070; KRINGLE\_2; 4.  
 KW Kringle.

FT NON TER 1 1  
 FT NON TER 359 359  
 SQ SEQUENCE 359 AA; 41172 MW; 776D35F4AB0BD9E CRC64;

Query Match 84.8%; Score 1306; DB 2; Length 359;  
 Best Local Similarity 81.2%; Pred. No. 1.3e-91;  
 Matches 211; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 1 VYLSECKTGKNGKRYGTMSKTKNGITCOKWSSTSPHRRPSPATHPSEGLSENYCRNPDN 60  
 |||  
 DB 1 VYLSECKTGKNGKRYGTMSKTKNGITCOKWSSTSPHRRPSPATHPSEGLSENYCRNPDN 60  
 |||

QY 61 DPGPMCYTTDPPEKRYDYCDILECEEECHMGSGENYDGIKSKTMSGLECOAMDSPHAA 120  
 |||  
 DB 61 DPGPMCYTTDPPEKRYDYCDILECEEECHMGSGENYDGIKSKTMSGLECOAMDSPHAA 120  
 |||

QY 121 GYIPSKFPKNIKKNKCRNPDELRPWCFTTDPNKRWEICDIPRCTTPPPSGPTTQCCLK 180  
 |||  
 DB 121 GYIPSKFPKNIKKNKCRNPDELRPWCFTTDPNKRWEICDIPRCTTPPPSGPTTQCCLK 180  
 |||

QY 181 GTGENYRGNAVAVYSGHTCOHWSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCYT 240  
 |||  
 DB 181 GTGENYRGNAVAVYSGHTCOHWSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCYT 240  
 |||

QY 241 TNSQVRWEYCKIPSCDSSPV 260  
 |||  
 DB 241 TNSQVRWEYCKIPSCDSSPV 260  
 |||

RESULT 4  
 PLMN RAT STANDARD; PRT; 812 AA.  
 AC 00117; O9R0W3;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Plasmalogen precursor (EC 3.4.21.7) [Contains: Angiotensin].  
 GN Name:Plg;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 NX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bangert K., Johnsen A.H., Thorsen S.;  
 RA "Rat plasmalogen: cDNA and gene structure."  
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 343-511 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91250378; PubMed=1645711;  
 RA Kanalas J.J., Makker S.P.;  
 RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a  
 RT receptor site for plasminogen."  
 RT J. Biol. Chem. 266:10825-10829(1991).  
 RL J. Biol. Chem. 266:10825-10829(1991).  
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as  
 CC a proteolytic factor in a variety of other processes including  
 CC embryonic development, tissue remodeling, tumor invasion, and  
 CC inflammation; in ovulation it weakens the walls of the Graafian  
 CC follicle. It activates the urokinase-type plasminogen activator,  
 CC collagenase and several complement zymogens, such as C1 and C5.  
 CC It cleaves fibrin, fibronectin, chondrospondin, laminin and von  
 CC Willebrand factor.  
 CC -1- FUNCTION: Angiotensin is an angiogenesis inhibitor that blocks  
 CC neovascularization and growth of experimental primary and  
 CC metastatic tumors in vivo (By similarity).  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;  
 CC higher selectivity than trypsin. Converts fibrin into soluble  
 CC products.  
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen  
 CC activators, both plasminogen and its activator being bound to  
 CC fibrin. Cannot be activated with streptokinase.



Query	Match	84.4% Best Local Similarity	Score 1299;	DB 1;	Length 812;
Matches 213;	Conservative 21;	Mismatches 24;	Indels 0;	Gaps 0	
FT	DISULFID	124	164	By similarity.	
FT	DISULFID	152	176	By similarity.	
FT	DISULFID	185	262	By similarity.	
FT	DISULFID	188	316	By similarity.	
FT	DISULFID	206	245	By similarity.	
FT	DISULFID	234	257	By similarity.	
FT	DISULFID	275	352	By similarity.	
FT	DISULFID	296	335	By similarity.	
FT	DISULFID	324	347	By similarity.	
FT	DISULFID	376	454	By similarity.	
FT	DISULFID	397	437	By similarity.	
FT	DISULFID	425	449	By similarity.	
FT	DISULFID	481	560	By similarity.	
FT	DISULFID	502	543	By similarity.	
FT	DISULFID	531	555	By similarity.	
FT	DISULFID	568	687	By similarity.	
FT	DISULFID	578	586	Interchain (By similarity).	
FT	DISULFID	609	625	Interchain (By similarity).	
FT	DISULFID	701	768	By similarity.	
FT	DISULFID	731	747	By similarity.	
FT	DISULFID	758	786	By similarity.	
FT	CONFLICT	418	418	A -> S (in Ref. 2).	
SO	SEQUENCE	812 AA;	90535 MW;	8C703C51A10EBCE CRC64;	
Query Match		84.4%;	Score 1299;	DB 1;	Length 812;
Best Local Similarity		82.6%;	Pred. No. 1e-90;		
Matches 213;	Conservative 21;	Mismatches 24;	Indels 0;	Gaps 0	
Qy	1	VYLSSEKTKNGKNGVGTMSKTKNGTTCCKMSSTSPHPRPSPAHPSBEGLEENYCRNP	60		
Db	98	VYLSSEKTIIGVGYGTWISKTKTGTCQMSDTSPPHVKYSPSTHPSEGLEENYCRNP	157		
Qy	61	DPQGPCYTTDEPKRYDCDILECEBCEBMSGSENYGKISKTMSSGLECOAMPDSPPH	120		
Db	158	DEGPGCYTTDDQRYEYCNIPCEBCEBMYSGKTKGSKTMSSGLECOAMPDSPPH	217		
Qy	121	GYLPSKFPKPKLKKVYCSNPDRRLPWCFTTDPKRWELCDIPRCTTPPSSGPTVQCL	180		
Db	218	GYLPAKFPKPKLKKVYCSNPDRRLPWCFTTDPKRWELCDIPRCTTPPSSGPTVQCL	277		
Qy	181	GTGENTRGVAVTVSGHGCQMSAOTPHTRKTRTEPNPCNKLIDENYCRANDGKAPWCH	240		
Db	278	GREENRGVAVTVSGHGCQMSAOTPHTRKTRTEPNPCNKLIDENYCRANDGKAPWCH	337		
Qy	241	TNSQVWEYCKIIPSCDS 258			
Db	338	TDSQVWEYCKIIPSCDS 355			
RESULT 5					
PLNM_PIG					
ID	PLNM_PIG	STANDARD;	PRT;	790 AA.	
AC	P06867;				
DT	01-JAN-1988 (rel. 06, Created)				
DT	01-FEB-1991 (rel. 17, Last sequence update)				
DT	25-OCT-2004 (rel. 45, Last annotation update)				
DE	Plasminogen (EC 3.4.21.7).				
GN	Name=PIG				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_Taxid=9823;				
RP	SEQUENCE OF 1-560.				
RA	Schaller U., Marti T., Roesseler S.J., Kaempfer U., Rickli E.E.;				
RT	"Amino acid sequence of the heavy chain of porcine plasmin. Comparison				
RT	of the carbohydrate attachment sites with the human and bovine				
RT	species."				
RL	Fibrinolysis 1:91-102 (1987).				
RP	SEQUENCE OF 450-790.				
RP	MEDLINE=85203907; PubMed=3846533;				
RA	Marti T., Schaller U., Rickli E.E.;				



RT "Determination of the complete amino-acid sequence of porcine miniplasminogen." Eur. J. Biochem. 149:279-285 (1985).

RL (3)

RP CARBOHYDRATE-LINKAGE SITES.

RX MEDLINE=89185329; PubMed=3356193;

RA Mari T., Schaller J., Rickli E.E., Schmid K., Kamberling J.P., Gerwig G.J., van Halbeek H., Vliegenhart J.F.;

RT "The N- and O-linked carbohydrate chains of human, bovine and porcine plasminogen. Species specificity in relation to sialylation and fucosylation patterns." Eur. J. Biochem. 173:57-63 (1988).

RL FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.

CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: N-linked glycan contains N-acetylglucosamine, sialic acid and diaccharide which is modified with up to 2 sialic residues (microheterogeneity).

CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.

CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily.

CC -1- SIMILARITY: Contains 5 kringle domains.

CC -1- SIMILARITY: Contains 1 PAN domain.

DR HSSP: P00747; PLPG.

DR MEROPS: S01.233; -.

DR GLYCOSITE: P06867; -.

DR InterPro: IPR000001; Kringle.

DR InterPro: IPR003014; PAN.

DR InterPro: IPR003609; Pan\_APP.

DR InterPro: IPR001254; Peptidase\_S1.

DR InterPro: IPR001314; Peptidase\_S1A.

DR InterPro: IPR003965; Peptidase\_S1A\_pr.

DR InterPro: IPR009003; Pept\_Ser\_Cys.

DR Pfam: PF00051; Kringle; 5.

DR Pfam: PF00024; PAN; 1.

DR Pfam: PF00089; Trypsin; 1.

DR PIRSF: PIRSF001150; Plasmin; 1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00018; KRINGLE.

DR PRINTS: PR01505; PROTHROMBIN.

DR PRODOM: PD000395; Kringle; 5.

DR SMART: SM00130; KR; 5.

DR SMART: SM00473; PAN\_AP; 1.

DR SMART: SM00020; Tryp\_Ser; 1.

DR PROSITE: PS00021; KRINGLE\_1; 5.

DR PROSITE: PS00070; KRINGLE\_2; 5.

DR PROSITE: PS50948; PAN; 1.

DR PROSITE: PS50240; TRYPSIN\_DOM; 1.

DR PROSITE: PS00134; TRYPSIN\_HIS; FALSE\_NEG.

DR PROSITE: PS00135; TRYPSIN\_SER; 1.

DR Blood coagulation; Direct protein sequencing; Fibrinolysis; Glycoprotein; Hydrolyase; Kringle; Plasma; Repeat; Serine protease; Tissue remodeling; Zymogen.

KM CHAIN 1 790 Plasmin heavy chain A.

FT CHAIN 561 790 Plasmin light chain B.

FT DOMAIN 1 79 PAN.

FT DOMAIN 561 790 Serine protease.

FT DOMAIN 84 162 Kringle 1.

FT DOMAIN 166 243 Kringle 2.

FT DOMAIN 256 333 Kringle 3.

FT DOMAIN 358 435 Kringle 4.

FT DOMAIN 461 540 Kringle 5.

FT ACT\_SITE 602 602 Charge relay system.

FT ACT\_SITE 645 645 Charge relay system.

FT ACT\_SITE 740 740 Charge relay system.

FT CARBOHYD 289 289 N-linked (GlcNAc...).

FT CARBOHYD 340 340 O-linked (GalNAc...).

FT SEQUENCE 790 AA; 86592 MW; F04E06E74BCD58E CRC64;

QY Query Match 83.9%; Score 1292; DB 1; Length 790;

Db Best Local Similarity 81.4%; Pred. No. 3 4e-90;

QY 1 VYLSECKTGNGKNYRGTMSKTNGITCKMSSTSPRRPFPSPATPSPSEGLEENYCNPN 60

Db 79 IYLSECKTGNGKNYRGTSTKSGVLCQKWSVSPHLPKSPKPLAGLEENYCNPN 138

QY 61 DPGPMCTTDPKRYDYCDILECECHGSGENTDKISKTMSGLEQANDSGSPHAX 120

Db 139 DEKPMCTTDPETRDYCDIPECEDECHGSGEHYEGKISKTMSGIEQSWGOSPHAX 198

QY 121 GYIPSKFPNNKLNKYNCRNPDRLEPWCFTTDPNKKWELCDIPRCTTTPPSGPTQCLK 180

Db 199 GYIPSKFPNNKLNKYNCRNPDRLEPWCFTTDPNKKWELCDIPRCTTTPPSGPTQCLK 258

QY 181 GTGENRYGNVAVTSGHTCOHWSAQTPTHERTPENPCKNLDENYCRNPDRGRAPWCHT 240

Db 259 GRENYRGVTSVYASHTCQMSAQSPPHNNRPENPCKNLEENYCRNPDRGTAPWCHT 318

QY 241 TNSQVMEYCKIPSCSS 258

Db 319 TDSVEMDYCKIPSCSS 336

RESULT 6

PLAN\_BOVIN STANDARD; PRT; 812 AA.

ID PLAN\_BOVIN

AC P06868; Q28162;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Plasminogen precursor (EC 3.4.21.7).

GN Name=PLG;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC NCBI\_TaxID=9913;

OX NCBI\_TaxID=9913;

RN [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Berglund L., Andersen M.D., Petersen T.E.;

RT "Cloning and characterization of the bovine plasminogen cDNA.";

RL Int. Dairy J. 5:593-603 (1995).

RN [2]

RN SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.

RP MEDLINE=85203906; PubMed=3846532;

RX Schaller J., Moser P.W., Danneberg-Muller G.A.K., Rosselet S.J., Kamper U., Rickli E.E.;

RA "Complete amino acid sequence of bovine plasminogen. Comparison with human plasminogen." Eur. J. Biochem. 149:267-278 (1985).

RL [3]

RN SEQUENCE OF 706-812 FROM N.A.

RP MEDLINE=85023311; PubMed=6148961;

RX Malinowski D.P., Sadler J.E., Davie E.W.;

RA "Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen." Biochemistry 23:4243-4250 (1984).

RN CARBOHYDRATE-LINKAGE SITES.  
 RP MEDLINE=8155329; PubMed=3556193;  
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamberling J.P.,  
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.P.,  
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine  
 RT plasminogen. Species specificity in relation to sialylation and  
 RT fucosylation patterns.";  
 RL Eur. J. Biochem. 173:57-63(1988).  
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as  
 CC a proteolytic factor in a variety of other processes including  
 CC embryonic development, tissue remodeling, tumor invasion, and  
 CC inflammation; in ovulation it weakens the walls of the Graafian  
 CC follicle. It activates the urokinase-type plasminogen activator,  
 CC collagenases and several complement zymogens, such as C1 and C5.  
 CC It cleaves fibrin, fibronectin, chondrospondin, laminin and von  
 CC Willebrand factor.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;  
 CC higher selectivity than trypsin. Converts fibrin into soluble  
 CC products.  
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen  
 CC activators, both plasminogen and its activator being bound to  
 CC fibrin. Cannot be activated with streptokinase.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: N-linked glycan contains N-acetylglucosamine and sialic acid.  
 CC O-linked glycans consist of Gal-GalNAc disaccharide which is  
 CC modified with up to 2 sialic acid residues (microheterogeneity).  
 CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin  
 CC immediately after dissociation from the clot.  
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 5 kringle domains.  
 CC -1- SIMILARITY: Contains 1 PAN domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, X79402; CA55939.1; -;  
 DR EMBL, K02935; AAA30714.1; -;  
 DR PIR, S45046; PLEO.  
 DR HSSP, P00747; 2PK4.  
 DR MEROPS, S01.233; -;  
 DR GlycoSuiteDB, P06868; -;  
 DR InterPro, IPR000001; Kringle.  
 DR InterPro, IPR003014; PAN.  
 DR InterPro, IPR009003; Pept\_Ser\_Cys.  
 DR InterPro, IPR001254; Peptidase\_S1.  
 DR InterPro, IPR001314; Peptidase\_S1A.  
 DR InterPro, IPR003966; Peptidase\_S1A\_pr.  
 DR Pfam, PF00051; Kringle; 5.  
 DR Pfam, PF00024; PAN; 1.  
 DR Pfam, PF00089; Trypsin; 1.  
 DR PIRSF, PIRSF001150; Plasmin; 1.  
 DR PRINTS, PR00722; CHYMOTRYPSIN.  
 DR PRINTS, PR00018; KRINGLE.  
 DR PRINTS, PR01505; PROTHROMBIN.  
 DR ProDom, PD000395; Kringle; 5.  
 DR PROSITE, PS00021; KRINGLE\_1; 5.  
 DR PROSITE, PS00070; KRINGLE\_2; 5.  
 DR PROSITE, PS00948; PAN; 1.  
 DR PROSITE, PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE, PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE, PS00135; TRYPSIN\_SER; 1.  
 DR Blood coagulation; Direct protein sequencing; Fibrinolysis;  
 KM Glycoprotein; Hydrolyase; Kringles; Plasma; Repeat; Serine protease;  
 KW Signal; Tissue remodeling; Zymogen.  
 FT SIGNAL 1 26  
 FT CHAIN 27 812 Plasminogen.

FT CHAIN 27 583 Plasmin heavy chain A.  
 FT CHAIN 584 812 Plasmin light chain B.  
 FT DOMAIN 29 105 PAN.  
 FT DOMAIN 110 188 Kringle 1.  
 FT DOMAIN 192 269 Kringle 2.  
 FT DOMAIN 282 359 Kringle 3.  
 FT DOMAIN 384 461 Kringle 4.  
 FT DOMAIN 485 564 Kringle 5.  
 FT DOMAIN 584 812 Serine protease.  
 FT CARBOHYD 315 315 N-linked (GlcNAc...)  
 FT CARBOHYD 315 315 /FTid=CAR\_000014.  
 FT CARBOHYD 365 365 O-linked (GalNAc...)  
 FT ACT SITE 624 624 /FTid=CAR\_000015.  
 FT ACT SITE 667 667 Charge relay system.  
 FT ACT SITE 762 762 Charge relay system.  
 FT CONFLICT 335 335 N->D (in Ref. 2).  
 FT CONFLICT 516 516 O->H (in Ref. 2).  
 FT CONFLICT 555 555 P->L (in Ref. 2).  
 FT CONFLICT 744 744 T->R (in Ref. 3).  
 SQ SEQUENCE 812 AA; 91216 MW; 38A6AA691E220946 CRC64;  
 Query Match 83.8%; Score 1291; DB 1; Length 812;  
 Best local similarity 80.8%; Pred. No. 4.2e-90;  
 Matches 210; Conservative 23; Mismatches 27; Indels 0; Gaps 0;  
 QY 1 VILSEKTKGNKKNKTKNGITCOQMSSTSPHRRPAPTHPSGLSENYCRNPDN 60  
 DB 105 IYLLSEKTKGNKKNKTKNGITCOQMSSTSPHRRPAPTHPSGLSENYCRNPDN 164  
 QY 61 DPQGFVCTTDPKRRYDYCDILCEBECBCHSGENYDGIKSTMSGLECOAQMSQSPH 120  
 DB 165 DENGWCYTTDPPDKRYDYCDIPECECDKCHSGENYDGIKSTMSGLECOAQMSQSPH 224  
 QY 121 GYIPSKPNKRLKKNYCNPNRRLRPWCTTDPKRNWLCIPRCTTPPSGSPYQCLK 180  
 DB 225 GYIPSKPNKRLKKNYCNPNRRLRPWCTTDPKRNWLCIPRCTTPPSGSPYQCLK 284  
 QY 181 GTGENYRGNVAVTWSGHTCOQMSAQTPTHTERTENPFCKRLDENYCNPNRGPCKAPWCHT 240  
 DB 285 GTGKNYGTAVVTSNGHTCOQMSAQTPTHTERTENPFCKRLDENYCNPNRGPCKAPWCHT 344  
 QY 241 TNSQVRMEYCKIPSCDSSPV 260  
 DB 345 TNSVRMEYCTIPSCSSPL 364  
 Db  
 RESULT 7  
 ID Q6TC10 PRELIMINARY, PRT, 466 AA.  
 AC Q6TC10  
 DT 05-JUN-2004 (TREMBLrel. 27, Created)  
 DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)  
 DE Angiostatin.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN (1)  
 RP SEQUENCE FROM N. A.  
 RC STRAIN=Kunming;  
 RA Qiao H., Tang B., Sun X.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AY424276; AAR07361.1; -;  
 DR HSSP, P00747; 1B2I.  
 DR GO, GO:0005615; C:extracellular space; TAS.  
 DR GO, GO:0006915; P:apoptosis; IDA.  
 DR GO, GO:0006917; P:induction of apoptosis; IDA.  
 DR GO, GO:0046716; P:muscle maintenance; IMP.  
 DR GO, GO:0007519; P:myogenesis; IMP.  
 DR GO, GO:0016525; P:negative regulation of angiogenesis; TAS.  
 DR GO, GO:0042246; P:tissue regeneration; IMP.



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CC -----

DR EMBL; J04766; AAA50168.1; -

DR EMBL; AF481053; AAM22156.1; -

DR EMBL; BC014773; AAH14773.1; -

DR EMBL; BC057186; AAH57186.1; -

DR EMBL; AY134430; AAN15805.1; -

DR PIR; A38514; PLMS.

DR HSSP; P00747; 1BUT.

DR MEROPS; S01.233; -

DR MGD; MG1.97620; P1g.

DR GO; GO:0006915; P:apoptosis; IDA.

DR GO; GO:0006917; P:induction of apoptosis; IDA.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR003014; PAN.

DR InterPro; IPR001254; Peptidase\_S1.

DR InterPro; IPR001314; Peptidase\_S1A.

DR InterPro; IPR003966; Peptidase\_S1A\_pr.

DR InterPro; IPR009003; Pept\_Ser\_Cys.

DR Pfam; PF00051; Kringle\_5.

DR Pfam; PF00024; PAN; 1.

DR Pfam; PF00089; Trypsin; 1.

DR PIRSF; PIRSF001150; Plasmin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR01505; PROTHROMBIN.

DR PRODOM; PD000395; Kringle; 5.

DR PROSITE; PS00021; KRINGLE\_1; 5.

DR PROSITE; PS00070; KRINGLE\_2; 5.

DR PROSITE; PS00948; PAN; 1.

DR PROSITE; PS00240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; 1.

DR PROSITE; PS00135; TRYPSIN\_SER; 1.

DR Blood coagulation; Direct protein sequencing; Fibrinolysis; Glycoprotein; Hydrolyase; Kringle; Plasma; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.

KW Signal; Tissue remodeling; Zymogen.

FT SIGNAL 1 19

FT CHAIN 20 812 Plasminogen.

FT CHAIN 20 581 Plasmin heavy chain A.

FT PEPTIDE 20 97 Activation peptide.

FT CHAIN 98 581 Plasmin short form of chain A.

FT CHAIN 98 7436 Angiotensin.

FT CHAIN 582 812 Plasmin light chain B.

FT CHAIN 20 98 PAN.

FT DOMAIN 103 181 Kringle 1.

FT DOMAIN 184 262 Kringle 2.

FT DOMAIN 275 352 Kringle 3.

FT DOMAIN 377 454 Kringle 4.

FT DOMAIN 481 560 Kringle 5.

FT DOMAIN 582 812 Serine protease.

FT ACT\_SITE 624 624 Charge relay system (By similarity).

FT ACT\_SITE 667 667 Charge relay system (By similarity).

FT ACT\_SITE 762 762 Charge relay system (By similarity).

FT DISULFID 49 73 By similarity.

FT DISULFID 53 61 By similarity.

FT DISULFID 103 181 By similarity.

FT DISULFID 124 164 By similarity.

FT DISULFID 152 176 By similarity.

FT DISULFID 185 262 By similarity.

FT DISULFID 188 316 By similarity.

FT DISULFID 206 245 By similarity.

FT DISULFID 234 257 By similarity.

FT DISULFID 275 352 By similarity.

FT DISULFID 296 335 By similarity.

FT DISULFID 324 347 By similarity.

FT DISULFID 377 454 By similarity.

FT DISULFID 398 437 By similarity.

FT DISULFID 426 449 By similarity.

FT DISULFID 481 560 By similarity.

FT DISULFID 502 543 By similarity.

FT DISULFID 531 555 By similarity.

FT DISULFID 566 687 Interchain (By similarity).

FT DISULFID 578 586 Interchain (By similarity).

FT DISULFID 609 625 By similarity.

FT DISULFID 701 768 By similarity.

FT DISULFID 731 747 By similarity.

FT DISULFID 758 786 By similarity.

FT CONFLICT 235 235 R -> H (in Ref. 1).

FT CONFLICT 525 525 G -> D (in Ref. 1).

FT CONFLICT 649 649 S -> L (in Ref. 1).

SQ SEQUENCE 812 AA; 90781 MW; 24173260E6A2FFD2 CRC64;

Query Match 83.1%; Score 1279; DB 1; Length 812;

Best Local Similarity 81.0%; Pred No. 3.5e-89;

Matches 209; Conservative 22; Mismatches 27; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYGTNSKNGITTCQWSSSTSPHRRPFPATPSSGLEENYCRNPN 60

DB 98 VYLSECKTGIGNGYGTMSRTSGVACQKMGATPHVNYNYSSTHPNGLSENYCRNPN 157

QY 61 DPGGWCCTTPBPKRYVCDILCEBECMGSGENYDGIKSTKSGLECCQAWDSQPHAH 120

DB 158 DEQGPWCYTTTPDKRYDCNIPCEBECMGSCGEYCKISKTWSGLCCQAWDSQPHAH 217

QY 121 GYIPKFPNKULKKNYCNPPELHPWCTTDPNKRWELOIPRCTTPPSSGPTVQCLK 180

DB 218 GYIPKFPKSKULKKNYCNPPELHPWCTTDPNKRWELOIPRCTTPPSSGPTVQCLK 277

QY 181 GTGENYRGNAVTVSGHTCOHMSAQTPTHTERTPENPCCKULDENYCNPPGKRAPWCHT 240

DB 278 GGENYRGVSVTVSGTKCQWSEBTPRHNRTPENPCCKULEENYCNPPGKRAPWCHT 337

QY 241 TMSQVMEYCKIPSCDS 258

DB 338 TDSQLRMEYCEIPSCSS 355

RESULT 9

PLMN\_ERIEU STANDARD; PRT; 810 AA.

ID PLMN\_ERIEU Q29485;

AC 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Plasminogen precursor (EC 3.4.21.7).

GN Name=PLG;

OS Brinnaceus europaeus (Western European hedgehog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Insectivora; Brinnaceidae; Brinnaceinae; Brinnaceus.

OX NCBI\_Taxid=9365;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=96025778; PubMed=7592597; DOI=10.1074/jbc.270.41.24004;

RA Law R.M., Boonmark N.W., Schwartz K., Lindahl G.B., Wade D.P., Byrne C.D., Fong K.J., Meer K., Patchy L., "The recurring evolution of lipoprotein(a).". Insights from cloning of hedgehog apolipoprotein(a).". J. Biol. Chem. 270:24004-24009 (1995).

RT [2]

RP REVISIONS.

RA Law R.M., Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, chondrospondin, laminin and von Willebrand factor.

CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa -> Arg-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.

CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen



Db	201	GIYPAKPSKNNKMYCRNPDESPRRCCTTDPBKNKMEVCDIPRCITVVIIVIIIIIF	260
Qy	167	-----TPPSSGFTYCLKGTGNGVGNVAIVYSGHTCOHWSAQDPHTHE	211
Db	261	IFIIPIFIIFIIIFIMMPLPLKSGSSL-----GRGENYAGFVSVTASGKTCORWSBPQTHRN	316
Qy	212	RTPEFPCGNLDNENCRNPDGKRAPKCHTNTSNVREXCKIPSCDS	258
Db	317	RTPEFPCGNLDNENCRNPDGETAPWCVTYTDLSQLRMEYCEIPSCGS	363
RESULT 11			
ID	PLNM_MACEU	STANDARD;	PRT; 806 AA.
AC	O18783.		
DT	25-OCT-2004 (Rel. 45, Created)		
DT	25-OCT-2004 (Rel. 45, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Plasminogen precursor (BC 3.4.21.7).		
GN	Name=PLG,		
OS	Macropus eugenii (Tamar wallaby).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.		
OX	NCBI_TaxID=9315;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RA	MEDLINE=96004511; PubMed=9342350; DOI=10.1073/pnas.94.22.11992;		
RT	Lawn R.M., Schwartz K., Patchy L.,		
RL	"Convergent evolution of apolipoprotein(a) in primates and hedgehog."		
CC	Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).		
CC	-1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as		
CC	a proteolytic factor in a variety of other processes including		
CC	embryonic development, tissue remodeling, tumor invasion, and		
CC	inflammation; in ovulation it weakens the walls of the Graafian		
CC	follicle. It activates the urokinase-type plasminogen activator		
CC	collagenases and several complement zymogens, such as C1 and C5.		
CC	It cleaves fibrin, fibronectin, thrombospondin, laminin and von		
CC	Willebrand factor (by similarity).		
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Lys- -Xaa > Arg- -Xaa;		
CC	higher selectivity than trypsin. Converts fibrin into soluble		
CC	products.		
CC	-1- ENZYME REGULATION: Converted into plasmin by plasminogen		
CC	activators, both plasminogen and its activator being bound to		
CC	fibrin. Activated with catalytic amounts of streptokinase (by		
CC	similarity).		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin		
CC	immediately after dissociation from the clot (by similarity).		
CC	-1- INVOLVES ONLY: In the presence of the inhibitor, the activation		
CC	involves only cleavage after Arg-576, resulting in 2 chains held		
CC	together by 2 disulfide bonds. Without the inhibitor, the		
CC	activation involves also removal of the activation peptide (by		
CC	similarity).		
CC	-1- SIMILARITY: belongs to the peptidase S1 family. Plasminogen		
CC	subfamily.		
CC	-1- SIMILARITY: Contains 5 kringle domains.		
CC	-1- SIMILARITY: Contains 1 PAN domain.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	the European Bioinformatics Institute. There are no restrictions on ways		
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL; AF012297; AAB65760.1; -		
DR	HSSP; P00747; 1BU1.		
DR	InterPro; IPR000001; Kringle.		
DR	InterPro; IPR003014; PAN.		
DR	InterPro; IPR003609; Pan_app.		

[illegible]

Db 98 IYLSDCSGNGRNVGTLSTKTSKITCQKMSDLSPHVNYABSKYPDAGLEKNYCRNPD 157  
Qy 61 DPGWCVTTTDEKRYDYCDILECEECNCGENYDGIKSTMSGLECQAMDSQSPH 120  
Db 158 DVKGFWCTYTNNDINREYCDVECEDECHGCGENYRGITSTESGICQWDSQSPH 217  
Qy 121 GYIPKFPKPKLKNKYCRNPDELPKWCCTTDPNKRWELCDIPRCTTPSSGPTVQC 180  
Db 218 EYIPKFPKPKLKNKYCRNPDELPKWCCTTDPNKRWELCDIPRCTTPSSGPTVQC 277  
Qy 181 GTGENYRGVAVTAVSGHTCQWMSAQTPTHTERTPENPCCKNDENYCNPPGKAPWCHT 240  
Db 278 GCGENYRGVAVTAVSGHTCQWMSAQTPTHTERTPENPCCKNDENYCNPPGKAPWCHT 337  
Qy 241 TNSQVREYCKIPSCDS 258  
Db 338 TNPDRQECYCAIPSCGTS 355  
RESULT 12  
Q6PBA6 PRELIMINARY; PRT; 818 AA.  
AC Q6PBA6; 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Plasmidogen.  
GN Name=PIG;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Alechuth S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usciti T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Ramey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smallegange D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Strausberg R.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC059801; AAH59801.1; -  
DR HSSP; P00747; 1B21.  
DR ZFIN; ZDB-GENE-030131-1411; pig.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0003809; F:trypsin activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0007596; P:blood coagulation; IEA.  
DR GO; GO:0006508; P:protein catabolic process; IEA.  
DR InterPro; IPR000001; Kringie.

DR InterPro; IPR003014; PAN.  
DR InterPro; IPR003609; Pan app.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR003966; Peptidase\_S1A.  
DR InterPro; IPR009003; Peptidase\_S1A.  
DR Pfam; PF00051; Kringie; 5.  
DR Pfam; PF00024; PAN; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00018; Kringie.  
DR PRINTS; PR01505; PROTHROMBIN.  
DR PRODOM; PD000395; Kringie; 5.  
DR SMART; SM00130; KR; 5.  
DR SMART; SM00473; PAN AP; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00021; Kringie\_1; 3.  
DR PROSITE; PS50070; Kringie\_2; 5.  
DR PROSITE; PS50948; PAN; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR Hydrobase; Kringie; Protease; Serine protease.  
KM SQUENCE 818 AA; 91635 MW; 55AC014BA38FF78 CRC64;  
SQ  
Query Match 64.7%; Score 996; DB 2; Length 818;  
Best Local Similarity 61.2%; Pred. No. 1,3e-67;  
Matches 158; Conservative 34; Mismatches 66; Indels 0; Gaps 0;  
Qy 2 YISECTGNGKNGYRGITMSKTGKITCQKMSSTSPHPRPSPATHPSEGLEENYCRNPD 61  
Db 106 YLLEFVNGIGMDYRGITMSKTGKITCQKMSSTSPHPRPSPATHPSEGLEENYCRNPD 165  
Qy 62 PGWCVTTTDEKRYDYCDILECEECNCGENYDGIKSTMSGLECQAMDSQSPH 121  
Db 166 KGGFWCTYTNNDINREYCDVECEDECHGCGENYRGITSTESGICQWDSQSPH 225  
Qy 122 GYIPKFPKPKLKNKYCRNPDELPKWCCTTDPNKRWELCDIPRCTTPSSGPTVQC 181  
Db 226 DVKGFWCTYTNNDINREYCDVECEDECHGCGENYRGITSTESGICQWDSQSPH 285  
Qy 182 GTGENYRGVAVTAVSGHTCQWMSAQTPTHTERTPENPCCKNDENYCNPPGKAPWCHT 241  
Db 286 EYIPKFPKPKLKNKYCRNPDELPKWCCTTDPNKRWELCDIPRCTTPSSGPTVQC 345  
Qy 242 TNSQVREYCKIPSCDS 259  
Db 346 TNPDRQECYCAIPSCGTS 355  
RESULT 13  
Q28398 PRELIMINARY; PRT; 2869 AA.  
AC Q28398;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Apolipoprotein(A) (Fragmant).  
OS Eritaceus europaeus (Western European hedgehog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.  
OX NCBI\_TaxID=9365;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=96025778; PubMed=7592597; DOI=10.1074/jbc.270.41.24004;  
RA Lamm R.M., Boommark N.W., Schwartz K., Lindahl G.E., Wade D.P.,  
RA Byrne C.D., Fong K.J., Meer K., Patsy L.;  
RT "The recurring evolution of lipoprotein(a). Insights from cloning of  
RT hedgehog apolipoprotein(a).";  
RL J. Biol. Chem. 270:24004-24009(1995).  
DR EMBL; U33170; AAC48522.1; -  
DR InterPro; IPR000001; Kringie.







